

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT  
GGTGGACAAGTTTAAACAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGCGGGAAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCGTGGTGGCTGCAGCTGAAGAGCGAATATCTGACTTATTCGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGGCGACGGGTCTGCGCGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCTGACGGCTTCGAAGAAAACG  
GAAGATGCCTGTGTGCCGCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT  
GCCCTCCCGCAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTTCAGAAGGATGTCC  
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA  
AACAGACTTGATATTTTGATACAGTTCTTTGTAATAAAATTGACCATGTAGGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCCGCGCACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCAACTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTCTACTGCATTCTAGTTGTGGTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG  
TGTGTCAAGTTAGGTTGTGAAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTT

## FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop  
><MW: 38192, pI: 4.53, NX(S/T): 2  
MRLPRRAALGLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLSESSSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWNLQLKSEYPDLFEWFCVKTLCVCCSPGTGYPDCLACQGGSGRPCSG  
NGHCSGDGSRGQDGSRCRCHMGYQGGLCTDCMDGYFSSLRNETHSICTACDESKTCISGLTNRDCGECEVGWVLDE  
GACVDVDECAAEPPFCSAAQFCNANGSYTCCECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAET  
CVRKNENYNTPGSYVCVCPDGFEEEDACVFPAAEAEATEGESPTQLPSREDL

### **Signal peptide:**

amino acids 1-24

### **N-glycosylation sites.**

amino acids 190-194 and 251-255

### **Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

### **Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

### **Tyrosine kinase phosphorylation site.**

amino acids 303-310

### **N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

### **EGF-like domain cysteine pattern signature.**

amino acids 166-178

### **Leucine zipper pattern.**

amino acids 94-116

## FIGURE 3

CAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCGCAGGCGGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTTCGCGGCAGCGAGGAGTCTCTGAGCAGCATGCCCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCTCTGTGCTGTGGCACTGCGGGCGGAGGC  
CGGGCCGCCGAGGAGGAGCCTGTACCTATGGATCGATGCTCACCAGGCAGAGTACTCA  
TAGGATTTGAAGAAGATATCTGATTGTTTTCAGAGGGGAAAAATGGCACCTTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC  
CTGGCAAGCTGCGAGGCGAGGAGAGATACTTCTATGAATTCCTGTCTTGGCGTCCCTGGGATA  
AAGCATATGCGAGATCCAAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA  
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAAAGGATGGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTTCTCCAAACACCTCAAAATGCTATCT  
TCTTTAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCTGTATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTGT  
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC  
TGTTTCTACCCTGGAATAATGATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAATCAG  
CAATGCCCCAACCCCTGTGCAAAATGGAGGTAATGCAATTGGTAAAGCAAATGTAAGTGT  
CCAAAGGTTACAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT  
GGAACCTGCCATGAACCCAAACAAATGCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAGGTACGAAGCCAGCCTCATAACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA  
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT  
TCATTATAAATCACTGAGCTGATATTACTCTTCTTTTAAGTTTTCTAAGTACGCTCTGTAG  
CATGATGGTATAGATTTTCTGTTTTCAGTGTCTTGGGACAGATTTTATATTATGTCAATTGA  
TCAGGTTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTAACAATGCATTTATGGT  
GTCTGGGGGCGAGGGGAACATCAGAAAGGTTAAATGGGCAAAAATGCGTAAGTCACAAGAA  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAGATTTTATTGTGAGATATTTAGAT  
GTTTGTACATTTTAAAAAATGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC  
TTACCATTATTTCCAGAGATTTCAGTATTAACAAAAAATAATTAACCTGTGGTAGTGGCATT  
AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACCTTTTGCAT  
TGGCTTGAAGCAATATAATATATTGTAACAAAAACACAGCTCTTACCTAATAAACATTTTAT  
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTTGGAAAAAATAAATAAATAAATAA  
AAAAAATAAATAAATAAATAAAGGCGCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

## FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094  
><subunit 1 of 1, 379 aa, 0 stop  
><MW: 41528, pI: 7.97, NX(S/T): 2  
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESSLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPIPVNIHSMNFTWQAAGQAEYFYEFSLRLSDKGIMADPTVNVPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC  
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST  
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICIGKSKCKCSKGYQGDLCSKPVC  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP  
PESNYIW

### Signal peptide:

amino acids 1-28

### N-glycosylation site.

amino acids 88-92, 245-249

### Casein kinase II phosphorylation site.

amino acids 319-323

### Tyrosine kinase phosphorylation site.

amino acids 370-378

### N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

### ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

### EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

# FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGACAGCCAGGAGCGGAGGCGCGGGGCCAGCCTGGG  
 CCCCAGCCCACACCTTCACACAGGGCCCAGGAGCCACC**ATGT**GGCGATGTCCACTGGGGCTAC  
 TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCACAGGGTTCGTGGGCGCCGG  
 GAGCTAGCACCCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCGCGGTACTGCCAGGA  
 GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
 GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
 TGCCTCGGCGTGCCACCCCTTTTCCCGGATCCAAGGATGTATGCATGGAGGTTCGTATCTA  
 TCCAGTCTTGGGAACGTACTGGGACAACCTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
 GGCATGGTGGATCCAGACATGATCAAAGCCATCAAACAGGGCAACTATGGCTGGCAGGCTGG  
 GAACCACAGCGCTTCTGGGGCATGACCTGGAT**GAGGG**CATTGCTACCGCGCTGGGCACCA  
 TCCGCCCATCTTCTCGGTTCATGAACATGCATGAAATTTATACAGTGTCTGAACCCAGGGGAG  
 GTGCTTCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCCAACCTGATTTCATGAGCCTCTTGA  
 CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
 CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCGAGAACCCTGCTGTCTTGTGAC  
 ACCCACCAGCAGCAGGGCTGCCGCGGTGGCGCTCTCGATGGTGCCTGGTGGTTCTTCGCTCG  
 CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC  
 CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCCGGGCAAGCGCCAGGCCACTGCC  
 CACTGCCCCAAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
 CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
 TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
 CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
 AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGGCAACTCCTGGGGCC  
 CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGGGCGTCAATGAGTGCACATCGAG  
 AGCTTCGTGCTGGGCGTCTGGGGCCGCTGGGCATGGAGGACATGGGTTCATCACTGAGGCTG  
 CCGGCACACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGCGGGAAGAGGCCCCCAATG  
 GGGCGGTGACCCAGCCTCGCCCGACAGAGCCCGGGCGCAGGCGGGCGCCAGGGCGCTAAT  
 CCGGGCGGGGTTCGCTGACGACGCGCCCGCCTGGGAGCCGCGGGGAGGCGAGACTGGCG  
 GAGCCCCCAGACCTCCAGTGGGACGGGGCAGGGCCTGGCTGGGAAGAGCACAGCTGCAG  
 ATCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
 CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG  
 TTGCCCCAGGTTGGAGTGCACTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
 AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACACACCTGGC  
 TAATTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAACT  
 CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCAAAGTGCTGGGATTGCAGGCATGAGCC  
 ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTATTTTCTTTTCACTGTTTTAAAA  
 TAAACCAAAAGTATTGATAAAAAAAA

## FIGURE 6

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPPFPIQGCMHGGRIYPVLGTYWDCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
```

### **N-glycosylation site.**

amino acids 78-82, 161-165

### **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

### **Amidation site.**

amino acids 26-30, 318-322

### **Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCTGGTGGTTCCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCACTGCCCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

## FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCACTAGCAAAGGCTG  
CAGCTTGAAGTCGCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGG  
CCCCGCTGCAGCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCTGGTTCTTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAAACCTCTCTGCTGCTGTTTC  
CATGGCCAGCATTTCCACCCTTAACCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT  
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCAGTTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAA



## FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPSPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVFPQASVPLLTDLAQWEPVLVPEAHPNASLTMVCTPVPHDPMPMALSRTPTRQISSSDT  
DPPADGPSNPLCCCFHGPAPFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

### **Signal peptide:**

amino acids 1-47

### **N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

### **N-myristoylation site.**

amino acids 56-60

### **Amidation site.**

amino acids 70-74

## FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCGCCCGCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAAGTACACGGGCGTTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC  
TCATAGTGGAGACGGACACGTTTGCCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG  
CGTGTTACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCCAGAACGCCCGGCACGAGG  
GCTGGTTCATGGCCTTACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGCGCCTTACCAAGGCCAGCTGCCCTTCCCCAACACGC  
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC  
GGCGGCCCCAGCCCTCACGTAGTCTGGGAGGCAGGGGCGAGCAGCCCTGGGCCGCTCCC  
CACCCCTTTCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCTGAGGGCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGAGGCCGGTG  
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGA  
GAGTGTACCCCTGATCTCAGGCCACAGCCTCTGCCGCTCCAGCCGGGCTCCTGAAGCC  
CGCTGAAAGGTGAGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCAACTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTTGTGTTGTTGTTGTTTTCAGGAAAAAAGAAAGGGAGAGAGGAAAAATAG  
AGGGTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCAACTCCCAGCCC  
CGGAATAAAACCATTTTCCTGC

## FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLIKPSGKSKDCVFTEIVLE  
NNYTAFQNRHEGWFMATPRQGRPRQASRSRQNRQEAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTTRRPQPLT

### **Signal peptide:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 9-13, 126-130

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

### **Casein kinase II phosphorylation site.**

amino acids 65-69

### **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

### **N-myristoylation site.**

amino acids 69-75, 188-194

### **Amidation site.**

amino acids 58-62

### **HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCCTCCTGTTGAATTTTTTGCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTTGATTTTTGCTGTTTATTTTTTTTTTCTTTTCTTTTTCCACCACATTGTATTTTAT  
TTCCGTACTTCAGAAATGGGCTTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCCT  
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCAGAGGTGCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGGAGGGGTAAACCGTACTCTACCTCCACAACACCAATTAATAATGC  
TGGATTTCTGCGAAGCTGCACAAATGTACAGTCGGTGACACGGCTCTACCTGTATGGCAACC  
AAGTGGAGCAATTTCCCATGAACCTTCCCAAGAATGTACAGAGTTCTCCATTGCGAGAAAA  
AATATTGACACCATTTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACTCCATATCCACAGTGGGGTGGAGACGGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTGGGGCTTCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTATTGTGGACGGGAACCTCCTGACCAACAAGGTATCGCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCAATTGTACGTAATTCGCTGTCC  
CACCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACAGAT  
AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTTTGTATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCTTGGTTTTGTGACTGCGAGTATTAATGGGTACAGAAATGGCTCAA  
ATATATCCCTTCATCTCTCAACGTGCGGGTTTTCATGTGCCAAGGTCTTGAACAAGTCCGG  
GGATGGCCGTGAGGGAATTAATATGAATCTTTGTCTGTCCCAACACGACCCCGGCTG  
CCTCTCTTACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCTCTCTAT  
TCCAAACCTTAGCAGAAGCTACACGCCTCCAACCTCTACCACATCGAAATCTCCACGATTC  
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACTTATTCTGAACGGATCCAGCTCTCTATC  
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCCACCGTGATGGCATA  
CAAACCTCACATGGGTGAAATGGGCCACAGTTTGTAGTGGGGGCATCGTTCCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACCTGAGCCTGGTTAACTTAGAGCCCGATCCACCTATCGGATT  
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCAATTGTTGAGAGGC  
CACCACCCATGCTCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCAAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTATATT  
GTGCTGGTGGTCTTGCTCAGCGCTTTTTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGGCGGCGGAAAGATGATTATGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTAGATCGTCTCTTAAATAACGAT  
CAACTCCTTAAAGGAGATTTCAGACTGCAGCCATTTACACCCCAATGGGGGCATTAAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAGGCGGACAAATTAGACTCTTGAGAA  
CACACTCGTGTGTGCACATAAAGACACGAGATTACATTGTATAAATGTTACACAGATGAT  
TTGTGCATTTGAATCTGTAAATTATACGGGTACTATATAATGGGATTAATAAAAAAGTG  
CTATCTTTTCTATTTCAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTAAATCTT

## FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRNDFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDNISITVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMVAVRELNMMNLLSCPTTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPITPDWDGRERVTPPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNRYRAVEDTICSEATHASYLNNGSNTASSHEQTTSMSGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

### **Signal peptide:**

amino acids 1-42

### **Transmembrane domain:**

amino acids 542-561

### **N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

### **Tyrosine kinase phosphorylation site.**

amino acids 319-328

### **N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

### **Amidation site.**

amino acids 581-585

### **Leucine zipper pattern.**

amino acids 164-186

### **Phospholipase A2 aspartic acid active site.**

amino acids 39-50

# FIGURE 14

ACTTTGGAGCAAGCGGGCGGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCACAGACG  
ATCCCCGAGGAGAGCGCGCGCCCTCGGCGAGGGCAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC  
TCGCTTCCGAGGCGCGGGCTCGAGCCTTGCCCTCTTGCTCGCTTGAAATGAGAAAGATGCTCGCAGGCT  
GCTTTCTGCTACTCTCGACAGATGCTCTCTCTCGGAGGCGAGGCGGTCAGCTGGGAGGTCCATCT  
CTAGGGGCGAGCAGCTCGGACCCACCGCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAAACAGCGGGCGAGCC  
TGSTTTTCTATCTTGACAGCTCTCGAGGTGTCAACACCCATGACTATGCAAAAGGTCAAGAGAGTTTCATCTGGACA  
TCTTTGCACTTCTGGACATTTGCTCTGATGTCAACCGAGTGGGCTGCTCAATATGGCAGCACTGTCAAGAAATG  
AGTCTCCCTCAAGACTTCAAGAGGAAGTCCGAGGTGGAGCGTGTCTGCAAGGATGCGGACATCTGTCCACGG  
GCACCATGACTGGGCTGGCATTCACTATGCCCTGAACATCGCATTCTCAAGAGCAGAGGGGGCCCGCCCTGA  
GGGAGAAATGTGCCACGGTCCATAATGATCTGTGACAGATGGGAGACCTCGAGACTCCGTGCGCCAGTGGCTGA  
AGGCACGGGACACGGGCTACTTAATCTTTGCCATTGGTGGGCGAGGTAGACTTCAACACTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTCTTTGTGCCAATTTGACGAGATTGAGACGCTGACCTCCGTGTCC  
AGAAGAAGTTGTGACGCGCCCATGTGTGCAGCACCTGGAGCATAACTGTGCCCACTTGTGCATCAACATCCCTG  
GCTCATACGCTGTGAGGTGCAACCAAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAACTCAGGATCTGT  
GTGCCATGGAGGACCAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCTTCTGTGTCCAGTGCTACAGTG  
GTACAGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCTCAGAAAAACCCAGATGTGAAC  
ATGAGTGTGAATGTGATGGCTCTTACCTTTGCGCAGTGCCATGAAGGATTTGTCTCTTAACCCAGATGAAAAA  
CTGTGCACAGGATCAACTACTGTGCATGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACTTGGAGGAGCT  
ACTACTGCCGTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACTCGACGCGGATGGACCACTGTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTGTGAACACGGAGGATTCCTTCTGTCTGCCAGTGCTCAGAAAGCTTCC  
TCATCAACAGGACCTCAAGACCTCTCCGGGTGGATTACTGCCCTGTGATGACCTGTTGTGAATCTCTCT  
GTGTCAACATGGAAGATCTTTGCTGTCTGAGTGTCTGTGAGGACAGCTGTCCGACGCGATGGGAAGACGTGTG  
CAAAATTTGACTCTTTGTGCTCTGGGGGACACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCTGTTGTGT  
GCCAGTGCTTTGAAGGTTATATCTCCGTGAAGAAGGAAAACTGCAAGAAAGAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGAACGACTATACAGCTGCGAGTGTCTGGAGGGATTCGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAACTCAACCCCAATGGCTGCCAAGACATTTGTGTTA  
ATAATGGGAATTCATACATCTGCAAAATGCTCAGAGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCCTGAAGGCCCAATTGACTGTGCTCTTTGTGATCGATGGATCAAGAGTCTTGGAGAAGAGAAATTTGAGGTGTG  
TGAAGCAGTTTGTCACTGGAATTTATAGATTCTTGTGACAAATTTCCCAAGGCCGCTCGAGTGGGGCTGCTCCAGT  
ATTCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCACTCAGCCAAAGACATGAAAAAGCCGTGGCCCC  
ACATGAAATACATGGGAAAGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAAGAAAGTTTACCCAG  
GAGAAGGGGCCAGGCCCTTTCCCAAGGGTGCCAGAGCAGCATTGTGTTCAACGACGAGCGGGCTCAGGATG  
ACGTCTCCGAGTGGGCGAGTAAGCCAAAGGCCAATGGTATCACTATGTATGTTTGGGGTAGGAAAAAGCCATTG  
AGGAGAACTACAAGAGATTGCTCTGAGCCCAACAAAGCATCTCTCTATGCCAAGACTTCAGCACAATGG  
ATGAGATAAGTGAAAAATCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGATCTCCAG  
CAGGGGAATGCCAAAAACGGTCCAAAGCCAAACAGAACTGTGAGCCAGTCAACATAAATATCAAGACCTACTTT  
CCTGTTCTAATTTTGTGCTGCAACAGGATATCTGTTTGAAGAAGACAACTTTTACCGTCTACACAAAAGCTTT  
CCCATTCAACAAACCTTCAGGAAGCCCTTTGGAAGAAAAACAGATCAATGCAAAATGTGAAACCTTATAATGT  
TCCAGAACCTTGCAACGAAGAGTAAGAAAAATTAACACAGCGCTTAGAAGAAATGACACAGAAATGGAAGCCC  
TGGAAATCGCTGAGATACAGATGAGAGATTAGAAATCGCGACACATTGTAGTCATTGTATCACGGATTACAA  
GAAACCTGGTTGGCCACAGAAACAAAGCAAGAGATACACATACTTGTATATAATTTATCTAGGAAAAAAATCTCT  
TCAGAACTCTAAGATGAATTTGACAGGTGAGAATGAATAAGCTATGCAAGGTATTTGTAAATATCTGTGACAC  
AACTTGTCTTCTGCTCATCTGCTTTAGTGTGCAATCTATTGACTATACGATAAGTTTGCACAGCTCTTACT  
CTGTGAAAGACTGCCATAGGAACTGTGTTTTTTGTACTGGACTTACCTTGTATATGTATGTGATGTGATGTG  
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTATACAAATATAAATCACCCTTACG

## **FIGURE 15**

MEKMLAGCPLLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFII  
 DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
 KRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMI VTDGR PQDSVAEVAAKARD  
 TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
 CAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDL CAMEDHNCQLCVNVPGSFVCCYSGYA  
 LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINYCALNKPGC  
 EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCCQSEGFLI  
 NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCP EGHVLRSDGKTC AKLDS CALGDHGCE  
 HSCVSSSEDSFVCCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA  
 EDGKCRRKDVCKSTHHGCEHICVNNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID  
 GSKSLGEENFEVVKQFVTGII DLSLTISP KAA RVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
 HMKYMGKGSMTGLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
 GITMYAVGVGKAIEEBELQEIA SEPTNKHLFYAEDFSTMDEISEKLKGI CEALSDSDGRQDS  
 PAGELPKTVQOPT ESEPV TINI QDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSP  
 EEKHDQCKCENLIMFQNLANEVVRKLITQRLEEMTQRMEALENRLRYR

### **Signal peptide:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 221-225

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
 781-785, 819-823, 866-870

### **N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
 639-645, 690-696, 752-758, 792-798

### **Amidation site.**

amino acids 314-318, 560-564, 601-605

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
 540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG  
 GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC  
 CATGATTTTCCCTCCCGGGGCCCTTGGTGACCAACTTGCTGCGGTTTTTTGTTCTCTGGGGCTGA  
 GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCAACCGGTGTCAG  
 GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGTACACCTTGACCGGGGAGGTGTCTTC  
 ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTCTCTCAAACAGAAAGAAAGGAGGATC  
 AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
 ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
 CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
 TAGAACTCAATGTACTGTTCTCCAGCTCCTCCATCCTGCGCTCTCCAGGGTGTGCCCCAT  
 GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
 GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGACCAGCATTAGATGTCTATCCGTG  
 GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
 AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
 AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGAAGTGGGGTTGCTGGCTGGGCTGGTCC  
 TCTGTACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
 ATTGCTCCCCGACCCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCCT  
 TTCCTCTGTCACTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCCTGGTGCAT  
 TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
 GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTTCTTCTCTGGCTTGAGCCG  
 CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC  
 CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTTATAAGGGTCACCTCTAGCAC  
 AGAGGCCTGAGTCATGGGAAAGAGTCACACTCTGACCCCTAGTACTCTGCCCCACCTCTC  
 TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGCTCCAGGAGACAGAAGGAGAAGAGGA  
 AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCTCTTATGAAGCCAGCTG  
 CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC  
 CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGT  
 ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC  
 TTATTTAAACATAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAA  
 TGTTTGTATGAAAAA



## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFPAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLEVSTGPGAA  
VVAGAVVGTLLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPPWPKSSDTISKNGTL  
SSVTSARALRPPHGP RP GALTPTPSLSSQALPSPRLPTTDGAHPQPI SP I PGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## FIGURE 18

CGCCACCCTGCGGCCACCGCCAAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTG  
TTGAATTGTTCCCTATACCTCAAATTTGCACCAAGACACCTTGCTCCCAAATGCAAAATGTGA  
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTCAAA  
TTTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAAATGCTAATTTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTTGTACCTGGCTTCAGATCCAGCAGTAACCA  
AGACAGGTTTATCACTAATGATGGAAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT  
TAGATAATGTCGTATAGCTGCAAAATATTAATAAACTTTAAACAAAAATCAGATCCATAAAAA  
GAACCTGTGGCTTTGCTCAAGAAGTCTATAGAAATTCGTGTACAGATCTTTCAACCAACAGA  
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAGAAGCAACA  
CTATCTCAGCCAAGGACACCTTTCTAACTCACTCTTACTGAATTTGTAAACCGTGAAT  
AATTTTGTTCAAAGGGATACATTGTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACCTCATGCACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC  
AAAAGACCACAGAGTTTGATACAAAATTCACCGGATATAGCTCTCAAAGTTTCTTTTTTGAT  
TCATATAACATGAAACATATTTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA  
AGAGTATTGGTCCCTTTGCTTCATCATCTGCACACTTCTATTGAAACCTCAAAAATTATGAT  
AATCTTGAAAGAGGAGGAAGATCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAAACCC  
ACCCACATTATATGAACCTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATA  
GGTATAGGAGTCTATGTGCATTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGCATACCTCAAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTTTGAATTTTGATGTCTCTGGTCCCTTCATGGTATTAAGATTATAATATTCT  
TTACAAGGATCACTCACTAGGAATAATTATTTCATGATTGTCTTGCCATATGCATTTTT  
ACCTTCTGGTCTTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG  
TAGCCTATTCTTGTGCAACTGTTTTTCTTGTGGGATCAATACAAAATCAATAAGCTCT  
TCTGTTCAATCATTTGCCGAGCTGCTACACTACTTCTTTTAGCTGCTTTTGCATGGATGTGC  
ATTGAAGGCATACATCTCTATCTCATTTGTGTGGGTGTCATCTACACAAGGGATTTTTGCA  
CAAGAATTTTTATATCTTTGGCTATCTAAGCCCCAGCCGTGGTAGTTGGATTTTCGGCAGCAC  
TAGGATACAGATATTATGGCAACAACCAAGTATGTTGGCTTAGCACCAGAAAACAACCTTATT  
TGGAGTTTTATAGGACCAAGCATGCCCTAATCATCTTGTGTAATCTCTTGGCTTTTGGAGTCAT  
CATATCAAAAGTTTTTTCGTCACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACA  
TAAGGTCTTGTGCAAGGAGGACCTCGCTCTTCTGTTCTTCTCGGCACACCTGGATCTTT  
GGGGTTCTCCATGTTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTACAGCTCAGCAATGC  
TTTCCAGGGGATGTTCAATTTTTTATTCCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTTCAAAAATGTCCCTGTGTTGTTTGGATGTTAAGGTAAACATAGAGAATG  
GTGGATAATTACAACCTGCACAAAAATAAAAAATCCAAGCTGTGGATGACCAATGTATAAAAA  
TGACTCATCAATTTATCAATTTATTAACCTACTAGACAAAAGTATTTTAAATCAGTTTTTCT  
GTTTATGCTATAGGAACCTGTAGATAATAAGGTAATAAATTATGTATCATATAGATATACATGT  
TTTTCTATGTGAATAGTTCTGTCAAAAATAGTATTGCAGATATTGGAAAGTAATTTGGTTTT  
CTCAGGAGTATATCATCTGCACCAAGGAAAGATTTCCTTCTAACACGAGAAGTATATGAA  
TGTCTTGAAGGAAACCATGGCTTGATATTCTGTGACTCGTGTGCTTGAACCTAGTCC  
CCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGAACATAAGAGAATGAAGGGGCAGA  
ATATCAACAGGTGAAAAGGGAATGATAAGATGTATTTTGAATGAACGTGTTTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAAAATAAGAATTGAAGAACACATTTTACCATTTTGTGAA  
TTGTTCTGAACCTAAATGTCCACTAAAACCACTTAGACTTCTGTTTGTCTAAATCTGTTCTT  
TTTCTAATATTCTAAAAAATAAAAAAAGTTTACCTCCACAATTGAAAAAATAAAAAA  
AAAAAATAAAAAAATAAAAAAATAAAAAA

## **FIGURE 19**

MKRLPLL VVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSNGVGTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTTEFVKTVNNFVQDRDTEVVWDKLSVNHRRTHLTKLMHTVEQATLRISQS FQKTTEFDT  
NSTDIALKVFFFDSDYNMKHIHPHMNMMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSI GPLL  
SSDNFLLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTTLSHRKVTD RYRSLCAF  
WNYSPTMTNGSWSSEGCETYSNETHTSCRCNNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCFSIIAGL  
LHYFFLAAFAWMCIEGIHLYLIVGVVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT  
TKVCWLSTENNFIWFSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVHVHASVVTAYLFTVSNAPQGMFIFLFLCLVLSRKIQEEYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA  
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACTGATTGTCTTGCCATATGCATTTTACCTTC  
TGGTTCCTTCAGTGAAATTCAAAGCACCAGGA

## FIGURE 21

GCTCCAGCCAAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCGCCGAAACCCGGCCG  
 CTAAGCGAGGCCCTCCTCTCCCGCAGATCCGAACGGCCTGGGCGGGGTCAACCCGGCTGGGA  
 CAAGAAGCCGCCGCTGCTGCCCGGGCCCCGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
 GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
 TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG  
 CCGCCGCGCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
 GGCACCTACAGCCCCGCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG  
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCAGTATGG  
 ATCTTGCGCGGCTCTGGCTGGCCGTGGCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC  
 ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCGGACGGCGTGTGGACTGCGCGCGGGGCG  
 CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCCGCTCTGCGGACCGTGGCCATCAAGGG  
 CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
 ACTCGGAGGAAGACTGTGCTTTGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
 TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
 CAGAGGCTTTCTCCACTCTCTCATTTCTGCCATGTGCCCATGGTCCAGAGGAGCGCTG  
 AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTTCGCCCTTGGAGACCGACAGCATG  
 GACCCATTTGGGCTTGTCAACCGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTTAACT  
 GAGACCATGCCCGGCCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGACG  
 TGCTTCTACAAGAAGCTCCTGAGTCCAGTCTGTGTTTGTGTTTGTAGGAAGAAACATCTAGAA  
 GTTGTACATATTAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
 CATAACATTGTAAGCCTGTAGCTTGCCAGCTGTGCGCTGGGCCCCATTCTGCTCCCTCGA  
 GGTGTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
 TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATCTCTAATTTTTTCTCATCACTTC  
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTTCAAGAACAGGTGATCCACTCTGTA  
 AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
 ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAAGTACTGGAGCAGGCATGGCCCCACCAG  
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC  
 CTGAGGCCAGTTCTGTCTAGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGCT  
 TTCCATCTCCAGCCCCACCAGCCCTCTGCCACCTCACATGCTCCCATGGATTGGGGCCT  
 CCCAGGCCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
 TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC  
 CCTTTCCCGACACTTGGTTTTCAACATGATATTATGAGTAATTTATTTTGATATGTACA  
 TCTCTTATTTTCTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAAGTTTG  
 TTTTGTATATTAAATGGAGTTTGTGTTG

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLLEIKAVLRRTVAIKGVHVSRYLCMGADGKMQLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES  
MFSSPLETDSMDPFGLVTGLEAVRSPSFKE

### **Signal peptide:**

amino acids 1-22

### **Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

### **N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGCCTCCTGCGCTCCTGCCGCCGGGACCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCGGGAAAGATGGCGGAGGAGAGCCGCCACCGCCTCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCGCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA  
AGAAGACTGTTTCTCCAGATTAGAGTGGAAGAAACTGGGTCGGAGTGTCTCCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAC  
CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC  
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTCCAGAAGAGTAATTCTTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCAGCCTGTAATCCAGCACTTTGGAAGG  
CCGCGCGGGCGGATCACGAGGTCAGGAGTCTTAGACCAAGTCTGGCCAATATGGTGAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAAATA  
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

## FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCVEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNNSVGYYRRCPGKRMQVDDLNISGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATMSENVQWLTPVIPALWKAAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230



# FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
 AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGACCTGGCAT  
 CATGCTGCTATTCTCGCAAAATGACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA  
 ATGAATTAATCAATCTCTATGACCATTATACATACCTCCACCTTCAAAAAGTACATCAATA  
 TTATATCATTAAAGGAAATAGTAACCTTCTCTTCCAAATATGCATGACATTTTGGACAAATG  
 CAATTGTGGCACTGGCACTTATTTCACTGAAGAAAACTTTGTGGTTCTATGGCATTCTATCA  
 TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGACTG  
 TGGAAATCCTTAAGGGCCCACTTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGGCACT  
 CCGAATTCATGTGCTATCTGGCCTAGCTATCCTACCTAGTAACAAGCTGTAGATAAAAAAG  
 TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCCTTGGTTTACACCCAGATCCATTTAT  
 ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGCTCTTTAACTTTCCAGCCAGATTGCC  
 AGCTAACACACAGATTTCTTCTCTACAGACTAACAAATATTGCAAAAATGGAATCTCCACAG  
 ACTTTCCAGTAACCTTACTGGCCTGGATTATCTCAAAACAAATTTATCTTCAGTCAACCAAT  
 ATTAATGTAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA  
 ACTGCCCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAATCTATATTAATCACAACT  
 TGCTTTCTACAATTTCACTGGAGCCTTTATTGGCCTACATAATCTTCTTCGAGCTCATCTC  
 AATTCAAATAGATTTCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT  
 TCTGATGATTGGGGAAATCCAAATTACAGAATCAAAGACATGAACCTTAAGCCTCTTATCA  
 ATCTTCGACGCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT  
 GGACTGGAAGAACTTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
 TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAAATCCTATTAAATGAA  
 TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATAGCT  
 GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTCGAGATTGAAGAAAAATAGAAGC  
 TACTAACAAACCTAGATTGCTTACATTACCCCCAATGCATTTTTCAGACTCCCCAAGCTGG  
 AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATTGGTACCATTGAGTCTCTG  
 CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCTCCGTTG  
 GATGAACATGAACAAAAACCAACATTCCGATTCTGAGGCCAGATTCTAGTGTTCGCTGGACC  
 CACCTGAATTCGAAGTCAGAATGTTCCGGCAAGTGCAATTTCAAGGACATGAGGAAATTTGT  
 CTCCCTCTTATAGCTCCTGAGAGCTTTCTCTTAATCTAAATGTAGAAGCTGGGAGCTATGT  
 TTCCTTTCACTGTAGAGCTACTGCGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG  
 GCAAAAACTTTGGCTTAATCCCTGACAGACAAGTTCTATGTCATCTTCGAGGGAACACTA  
 GATATAAATGGCGTAACCTCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT  
 TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTCCACAAGATAACAATG  
 GCTCTTTGAATATAAAAATAAGAGATATTCAAGGCAATTCAGTTTGGTGTCTCGGAAAGCA  
 AGTTCTAAAATCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTTCTCA  
 TGCTGCGCAAGTGCTCGAATACCATTCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
 CATCAACTGAGTATAAAATTTGTATTGATATTCCCACCTATCTATCAGAAAAACAGAAAAAA  
 TGTGTAAATGTCAACCAAAAGGTTTGCACCTGATCAAAAAGAGTATGAAAAGAAATAATAC  
 CACAACACTTATGGCCTGTCTGGAGGCCTTCGGGGATTATTGGGTGTGATATGCTCTTATCA  
 GCTGCCCTCTCTCCAGAAATGAACGTGTGATGGTGGACACAGCTATGTGAGGAATTTACTACAG  
 AAACCAACCTTTGTCATTTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAA  
 AGAAAAAGTACATCACTGAAGTAAAAAGCAACTGTATAGTTTACCAACAAATATGTCTCT  
 AAAAACCACCAAGGAAACCTACTCCAAAAATGAAC

## FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA  
LPNLIELMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVVNLKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNLSNALSALYHGTIESLPNLKEISIHNSPIRC  
DCVIRWMNMNKTNI RFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSSVKWTAFV  
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPERMNCDGGHSYVRNYLQKPTFALGELYPPPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

### Signal sequence:

amino acids 1-22

### Transmembrane domain:

amino acids 633-650

### N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### Tyrosine kinase phosphorylation site.

amino acids 570-579

### N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### Cell attachment sequence.

amino acids 277-280

## FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAAACCTTTAC  
CAGCCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCCTTCCCTCTCCATGTGTCTCCTCTACAAAGTTTTGTTCCTTA  
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCCTGCG  
GGTTTAAATGTCACCTGTAGCAATGCAAAATCTCAAGGAAATACCTAGAGATCTTCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAACGTCCTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGCTGGTTCATATGGTGATCTCATATGTGGTATATATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCTATTGAGAAAGAAAGAAA  
GTAGTTTTCGATTGCAGTAGAAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTTGTATTTTCAAGTTTTTTTGAATTATGCCACTGTGAACTTTTAAACAAACTACAACA  
TAAATAATTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT  
AATTTAAAGCAATAAAGCTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

## FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTCSNANLKEIPRDL  
PPETVLLYLDNQITSIPNEIFKDLHQRLVNLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVIC KTSVLDEHAGRPFLL  
NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLSRQKK  
ADEPDDISTVV

### **Signal sequence:**

amino acids 1-33

### **Transmembrane domain:**

amino acids 205-220

### **N-glycosylation site.**

amino acids 47-51, 94-98

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

### **Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

### **N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

# FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATG CAGGTGAGCAAGAGGATGCTGGCGGGG  
 GGGCTGAGGAGCATGCCCAGCCCCCTCTGGCCTGCTGGCAGCCCATCTCTGCTGGTGT  
 GGGCTCAGTGCTGT CAGGCTCGGCCACGGGCTGCCGCCCGCTGCGAGTGCTCCGCCAGG  
 ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG  
 ACGCCGCTCTGTGACCTTAGGCAAGAACCGCATCAAAACGCTCAACCAAGGACGAGTTCGCCAG  
 CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCG  
 CTTTCAACAACTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC  
 CCGCTAGGCGTCTTCACTGGCCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT  
 CGTTATCTCTACTGGACTACATGTTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
 ACAATGACCTCGTCTACATCTCTCACC GCGCTT CAGCGGCCCTCAACAGCCTGGAGCAGCTG  
 ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGGCCT  
 CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCTTCAAGAGGC  
 TGTACCGACTCAAGGCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCCAAC  
 TGCCTCTACGGCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
 CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTTCAACCTCTCTTACAACCCCATCA  
 GCACATTGAGGGCTCCATGTTGCATGAGCTGCTCCGCTGCGAGGAGATCCAGTGTGGTGGG  
 GGGCAGCTGGCCGTGGTGGAGCCCTATGCCCTCCCGCGGCTCAACTACCTGCGCGTGTCTCAA  
 TGTCTCTGGCAACCAAGCTGACCAACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG  
 AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCTGTGGGTGTTCCGG  
 CGCCGCTGGCGGTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCGCGAGTTTGTCCA  
 GGGCAAGGAGTTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACTGCGCGCGG  
 CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACAGGGGCCACACGGTGCAGTTT  
 GTGTGCCGGGCGATGGCGACCCGCGCCGCGCATCTCTGGCTCTCACCCCGAAAGCACT  
 GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT  
 ACGCCAGGTACAGGACAACGGCAGCTACCTGTGCTATCGCGGCCAACGCGGGCGGCAACGAC  
 TCCATGCCCCCACCCTGCATGTGCGCAGCTACTCGCCGACTGGCCCATCAGCCCAACAA  
 GACCTTCGCTTTTATCTCCAACAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG  
 TGCCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTATCTCTTTC  
 CTGGGCGTGTCTCTTCTGCTGGTGTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC  
 AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGAGCAGGACATCAGTCCCGCG  
 ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGGCGGGGCGAGGACCCCCG  
 GGCGGCGGGGAGGGGAGGGGCGTGGTCCGCACTGCTCACTCTCCAGTCTTCCCACCTC  
 CTCCTACCTTCTACACACGTTCTCTTCTCTCCCTCCCGCTCCGTCCTCTGCTGCCCCCG  
 CCAGCCCTCACCACTGCCCCCTTCTTACCAGGACCTCAGAAGCCCGAGACCTGGGGAGCCCA  
 CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAAACCCGAGCCGCGGAGGATCA  
 ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTT  
 TATGAAACCTGGAATATAAAAAAGAAAAAACTAAAAA

## **FIGURE 30**

MQVSKRMLAGGVSRMPSPLLACWQPIILLVLGSLSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFLNRTL  
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA  
FSGLSLEQLTLEKCNLTSIPTAELSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKVLEISH  
WPLYDTMTPNCLYGLNLTSLSTHNCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTLEESVFHSGVGNLETLILDSNPLA  
CDCRLLWVFRRLNLFNRQQPTCATPEFVQGEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNRGLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVFLCLVLLFLWSRGKNTKHNIIEYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCAGCCCCGGGGATTCAAGGCTCGCCAGCGCCAGCC  
AGGGAGCCGCGCGGAAGCGCGATGGGGGCCCCAGCCGCTCGCTCTGCTCCTGCTCCTGCG  
TGTTCCGCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCTCAAGTGCCAAAGTGAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCTGTCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGTCTCAATCTTCACTATGCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCCGGCTCACTGGAGAAAGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGGTGCACAGCCACCAG  
CAACATGGGCAGCTACAAGGCCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCT  
CCTCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTTCATTGTCTTCTCTGCTG  
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCACTTCTCTGC  
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGACAGAGCAA  
CCGCGAGGGCCGCCCTCCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTTGTACTCGGTTTGAATGGGGAGGAGGGCGGGGGAGGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTTGGGTTATTATTATTTTGTAAACATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACA  
AACAAAAACA

## FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETIVVAGGTVVVKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRILVTSTPHELSSISISNVALADEGEYTCSTFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLHLHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTTCTCCTTTCTCGG  
CTTCGGACATTGGAGACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTTGGATCGAGATCGGGGATGAATTGCTCGCTTTAAAAAATGCTCCTGCTTTGGATTCTGTT  
GCTGGAGAGCTCTCTTTGTTTGGCCGCTGGAACCGTTACAGGGGACGTTTGCAGGAGGAA  
TCTGTTCTGTCAATGAGATAGAAAGGGGACCTACAGTACTGTGAAAAAAGGGCTTCACA  
AGTCTGACGCTTTCAGCTGCCCGGACTTCCAGTTTACCATTATTATTCTGCATGGCAATTC  
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGACATGG  
AAAACAATGGCTTGCATGAAATCGTTCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAAAGCTGCC  
CTATGAGGAGTCTTGAGCAAAATCCCTGGTATTGCGGAGATCTGCTGATAGGATAACCCCT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAAACATTCCCAAGAATGCC  
CTGATCGGGCGAGTGGTCTGCGAAGCCCCCAGCAGACTCGAGGGTAAGAGCCTCAATGAAAC  
CACGGAACAGGACTTGTGCTCTTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGGCCCTTG  
CCCCAAGAAGAGACTTTGCTCTCGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG  
GATCATGCCACACAGGGTCTGCTCCAAACGGAGGTACAAAGACTCCAGGCACCTGACGAT  
CAAAATCAGACCCACAGCAGCGATAGCGAGGGTAGCTCCAGGAAACAAACCTTAGCTAACA  
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCATCCAGGGTCGGGTTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTGGAAGCCCAAGCTCTCTAACGTGACGA  
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAATCGCACTTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACACACTTTCAAG  
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA  
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCCGGCACTTTCAATGCCATGCCAACTGAGGATCTCTACTTCTCAACAACAACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA  
CAATTACTTTCATGACTCTCCCGGTGGCAGGGGTGCTGGACCACTTAACTCCATCATCCAGA  
TAGACCTTCACGGAAACCCCTGGGAGTGCTCTGCACAAATGTGCTCCTTCAAGCAGTGGGCA  
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGAGCGCCGCTGAACTTCTT  
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCACGTTAACTTCCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACTCC  
AACTCCTACTAGACACCGCAGGGGTGCTCATCTCGGTGTGGTCCCGGGACTGCTGCTGGT  
GTTTGTCACTCCGCTTACCCTGGTGGGCATGCTCGTGTATCTGAGGAACGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCGCTCCGAGATTAATCCCTACAGACAGTCTGT  
GACTCTTCTACTGGCACAATGGGCTTACAACGAGATGGGGCCACAGAGTGTATGACTG  
TAGGCTCTACTCGCTCTCAGATTAAGACCCCAACCCCAATAGGGGAGGGCAGGGGGAAGGGC  
ATACATCCTTCCCCACCGCAGGACCCCGGGGGCTGGAGGGGGGTGACCCAAATCCCCGGC  
CCATCAGCTCGGATGGCAGTAAAGTAGATAAATACTGTGAGCTGCAACACGAAAGGGCT  
GACCCCTTACTTAGTCTCCCTCCTTGAACAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA  
GCCAGCTCGCTCTTGTGTGAGAGCCCTTTTGACAGAAAGCCAGCAGACCTGTCTGGAAG  
AAGTACAGTCCCTCGCCTCGCCCTCGCCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTGGCTACGCGAGGATGGGCACTTGACGGAAGGCATGAATGTAT  
TGTAATAAGTAACCTTGACTTCTGAC

## FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKSCNEIEGDLHVDCEKKGFTSLQRFTAPTSSQFYH  
LFLHGNSLTRLPNEFANFYNAVSLHMENGLHEIVPGAFLGLQLVKRLHINNKKISKFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLLEVLINDNLISTLPANVFQYVPIITHDLRG  
NRLKTLPEYEEVLEQIPGIAEILLEDNFPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCLPKNRVDSSLPAAPAEETFAPGPLETPFKTNGQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANS LCPFGGCS CDHIPGSGLKMNCNNRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLLEYLNVEYNAIQLILPGTFNAMPKLRILINNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDBICPQLYARISPTLTSHSKNSTGLAETGTHSNLYLDTSRVSI SVL  
VPGLLLVFVTSFTVVGMLVFILRNKRKSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 618-638

### **N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

### **Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### **N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCAGAACTCAGGGC  
TGCACCGGGCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGC  
CGCTGGGGCCCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGGAAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGGGGGCTCAG  
AGAATGAGGCGGGCGTTGCGCTGTGCTCTCTGGCAGGCGCTCTGGCCCCGGGCGGGCGG  
CGGCGAACACCCCACTGCCGACCGTGTGCTGCTCGGCTCGGGGGCTGTCTACAGCCTGC  
ACCAAGCTTACCATGAAGCGGCGAGGCGGCGAGGAGGCTGCACTCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTGCGCTCTGCGGGCAGGCCAGG  
GCCCGGAGGGGCTCCAAAGACCTGTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT  
GCACCTGGAGAACGAGCCTTTGCGGGGTTCTCTGGCTGTCTCCGACCCCGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCTGACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTGCAGCGCCGAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCGCGCCCCGGG  
GCCGCTCTAACTTGAGCTATCGCGCGCCCTCCAGCTGCACAGCGCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCGCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGAGCAAACTCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTCTCCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTTGGGAGG  
CTTTGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA  
GTGGGGAAGGACAGCCGACCTTTGGGGGACCGGGGTGCCACCAGGCGCCGCGGCCACT  
GCAACCGACCCCGTGCCGCGAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC  
ACCACTTGTCCCTGAACAAGACAATTGAGTAACATCTATTCTGAGATTCTCGATGGGGAT  
CACAGAGCACGATGTCTACCTTCAAATGTCCCTTCAAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTTCAAAGTTAATTCTACGACTTCTCTGCCACTCCTCAGGCTTT  
CGACTCTCTCTGCGCGTGGTCTTCAATTTGTGAGCACAGCAGTAGTAGTGTGTTGATCT  
TGACCATGACAGTACTGGGGCTGTCAAGCTCTGCTTTACGAAAGCCCCTCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCCCGCGGGCTGGAGAGTGATCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCCGGGACTGTGATCTGCGGGACAGAG  
CAGAGGTGCTTGTCTGGCGGAGTCCCCTTTGGCTCTAGTGATGCATAGGGAACAGGGGA  
CATGGGCACTCTGTGAACAGTTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTAC  
TTGTGTAAGTACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCTTCCCTGATGATAGAGGAAGTGGAAGTGCCCTTAGGA  
TGCTGATACTGGGGGACCGGTAGTGCTGGGAGAGATATTTCTTATGTTTATTCGGAGAA  
TTTGGAGAAGTGATTGAACCTTTTCAAGACTTGGAAACAAATAGAACCAATATAATTTACA  
TTAAAAATAATTTCTACCAAAATGGAAGGAATGTTCTATGTTGTTGACGCTAGGAGTAT  
ATTGGTTGCAATCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

## FIGURE 36

MRPAPALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSC TARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIAD EIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDG RSCVTS GEGQPTLGGTGVPTRRPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDN SVT SIPEIPRWGSQSTM TLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTM TVLGLVKLCFHESPPSSQPR  
KESMPPGLESDPEPAALGSSSAHCTNNGVKVGD CDLRDRAEGALLAESPLGSSDA

### Signal sequence:

amino acids 1-16

### Transmembrane domain:

amino acids 399-418

### N-glycosylation site.

amino acids 189-193, 381-385

### Glycosaminoglycan attachment site.

amino acids 289-293

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

### Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

### N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

# FIGURE 37

CGGACGCGTGGGATTAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCTCAGGGGAACTAAG  
 CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAGTGCCCTCGCCCTGCCGGCCGCGTATC  
 CCCCGGCTACCTGGGGCGCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGCGAGCCGA  
 GCGCGCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGCGGTGTGAGCGCGGTGGGTGCGGA  
 GGGCGGTGTGTGCCGGCGCGCGCGCGGTGGGGTGCAAAACCCGAGCGCTCTACGCTGCCATGA  
 GGGGCGCGAACGCGCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
 CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
 TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCGCCAAATAGCAAATGTACTTGGAAAAATCA  
 CAGTTCGCCGAAGGAAAAGTAGTCGTCTCAATTTCGATTTCATAGACCTCGAGAGTGAACAAC  
 CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCGG  
 CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
 TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
 AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCGGGCTCTTTAAAC  
 CCCCACCTGGCCAGACCGGGATTACCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC  
 CAAAGAATCAGCTTATAGAATTAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGCG  
 CGATATGATTATGTGGCTGTGTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
 GTATTGTGGTGATAGTCCACCTGCCCAATGTGTCTGAGAGAAATGAACCTCTTATTCACT  
 TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA  
 AAACCTGCCTACAACACAGACCTGTCAACCACCATTCCTCTGTAACACGGGTTTTAAA  
 ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGAGCTCTGGAGGGCAATTATT  
 GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAAACATCACTCGCGATGGGAGTTTG  
 CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACAGAGCGCGG  
 CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCTCAGAAGAGGTC  
 TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAACAGC  
 TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG  
 TTAACAGTGAACTGTGTCCATTAAAGCTGTATTCTGCCATTGCCCTTTGAAAGATCTATGTTC  
 TCTCAGTAGAAAAAAATACCTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
 GACTGGTTGACTCTTACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAGTTCTT  
 TGCTGCTGTGAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA  
 AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTATTTATACATCTCTGTAAAAGGAT  
 ATTTTGAATTTGAGTTGTGTGAAGATGTCAAAAAAGATTTTGAAGTGAATATTATAGT  
 GTTATTTGTTTACCCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGGCTTTTCTA  
 AATCAATGCTTAAATAAATATTTTAAAGGAAAAA

## FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFVTCGGILTGESGFIGSEGFPGVYPNSKCTWK  
ITVPEGKVVVNLNFRFIDLESNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEFNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTITTFPVTTLGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTACATCTG  
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG  
GTGAAACACTGCCTGGGAGGAAGAGAAATTGTCCAAATACAAGACAGTGAGACCCGCGCTG  
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGGCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGAGAGCTGGTGGTTTCAAGCAGCAGGAGGCCCCGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGCCACTGTGACTGCCAAGCGGCTACGGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTTGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTCCGGCTGT  
TTTGGCCCCGTGTGCCGATGCTCAGGACCTGAGGAATCAAATGTTTGTCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCAGAGGGAGCCAACT  
GTGGAGCTGACCAATTCTGCTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAACCCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCAATGGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTGAGAGCGAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGTAGAGTGGGGTAAGCACCCGTACCTG  
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTTGGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCAATGTGTGA  
ATTTCAAAAGTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCGTGTTAGGATTAGGTG  
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT  
TCTGTGTTACACCATCCCCACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA  
AAGGTCTTGAAAGTTAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLGVCSKSDFECHRLLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLP CGGTERPCGGYGQCEGEGTRGGSGHCDCQAG  
YGGEACGQCGLGYFEARNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDDIDE  
CGTEGANCGADQFCVNTGEGSYECRDCAKACLGC MGAGPGRCKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRICAEGYQKMEGICVKEQIPESAGFFSEMTEDELVV LQQMFFG  
IIICALATLAAKGD LVFTAFIGAVAAMTGYWLSERSDRVLEGFIKGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193



## FIGURE 41

TGAGACCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT  
GCCCCACCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT  
ACGTGGCCCTGTCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACCTGCTGGTGTTTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGACAGGCCGTGCTGCGGCTCTTCCAGG  
AGCCGGTCCCCAAGGCCGCTGTCACAGGCACGGCGGCTGTCCCCGCGCAGCGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCGTCCGTCACGAGAGCGGCTGGAAGGCCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGACAGAG  
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTCCTCGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGCGAGCCCCGGAGGCCCTGGCCCTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCGAGAA  
GTGCAGCTGTGCCCTCGGATGGTGCGCTCGTGCCAAGGAGGCTCCAGCCATAGCGCCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTTCGAGGGTACCAAGGAGAGCTG  
GCGATGACTGAAGTGTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTTGTCTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCTTGTGTTTACTTGTCTGTCTAC  
TGGATCTGGGCTAAAGTCTCCACCACCCTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAAGACTTGTGAAAACATGAATAAAACACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTRPPEALAFKWP  
LGPRQCIASETSLPMIVSIKEGGRTRPQVVS L PNM RVQKCSASDGALVPRRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTCACTGGCCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGAAGTCTTCTGAACCTGAAGTCAGAATTCCTGAGAAATAATCCT  
GTGAAGTTGTCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACCTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCTTACAGTTAACATCCCCCTCTCTGCCACCATTTGGGAACCGGG  
CAGTGTGACATGCTCAGAACAAAGATGGTTCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTCT  
GAATCCCAACACAGGAGAGCTGGTCTTTGATCCCTGTGAGCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCCATGGAAGCT  
GTGGAGCGGAATGTGGGGGTATCGTGGCAGCCGTCTTGTAACCTGATTCTCTGGGAAT  
CTTGGTTTTTGGCATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGTTCGGCTACCGCCTATCATCTGCATTGGCCTTACT  
CAGGTGCTACCGACTCTGGCCCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTCCCTACCACTGCTGAGTGGCTGGAACCTGTTTAAA  
GTGTTTATTTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAATGGCGGGGTCGAGGAATCTGCACTCAACTGCCCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCTTGTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAATGGGAGCTCTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACCTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAAGAAACTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGGAGTTCGGGATCAGCCTGACCA  
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPFVKLSLAYSGFSSPRVEW  
KFDQGDTRRLVCYNKKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTTPMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGCGGAACAGGGGCTCTGGGCGCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCCGCGAGCCCGCTTTCACCCCGACCTCTGCCCAGGCCGCGAGGCCCCAGCTCAG  
GCTCGTGCCACCCACCAAGTTCAGTGCCGCACCAAGTGGCTTATGCGTGCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCGAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCTGCCCCTGACCCGGCGTCA  
GTGACTGCTCTGGGGGAAGTACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTGCGGAATGCCACATCCTC  
CTCTGCCGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGTGCTGCGGTGC  
TCAGTGCAAGCCTGGTACCGGCCACCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC  
CTCGTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGAACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCACTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCTGTCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLLLLGLGLEAAASPLSTPTSQAAGPSSGSCPPTKFCQR  
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCCTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 230-246

### **N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

### **Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

### **N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

### **Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATTCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
CGATGACCTTCAAGTGTGTGTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCAGTCCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTTTAATGGAACCTAGGCTGGATCCCAAGTGA  
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTGATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGTGTCTTCCCGGATTAAACTT  
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTGTGCTCCAGCCACCCCGGTG  
CCTGTCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTACGGAGATTTCGTCT  
GCCACCCGCGCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTTACTGCGATCCT  
GGCTACAGCCTCACAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCTCCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAAGTGTGCTGTGTTGCTGTCTGTCTGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGAG  
TTCCAGCAGTGACCTTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCTTACCGGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA  
CACAGGCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA  
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCTTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCCCACTGGGT  
GTTGTTCTAAGAACTGATTGATTGATTAATAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCTTCTCTCTTGGTTTTAGACAAATGTAACAA  
AGCTCTGATCCTTAAATTGCTATGTCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKIITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFAHFPPRGPPRSSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQCPLPVDDQSPPAYPGSGD TDTGPGSESETCDS  
VSGSSELLQSLYSPRCQESTHPASDNPDI IASTAEEVASTSPGIHHAHWLFLRN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405



## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCTAGAGA  
TGCTGCTGCCCGGGTTGCAGTTGTTCGCGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCGT  
AGCGCCCGAGTGTCCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA  
TAAAGTCATTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA  
AAGTTCAATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT  
CACAAATTAGGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA  
CCGGTGCAACATGAAGAACAAATTTCAATTTGCAAATATTCTGATGAGAAACCGAGTTTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCTTGTGGTCAACCAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC  
TGGCCCTCTCCTCACCAGGGAACAGCCCGACCTAGAGGTCTACAATGTCATAAGAAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAAATATTTCAATCCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGAGAGTGGATTGTGACCAATGACATTTATGA  
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAAAAAGTAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTTGGCTGTATCCTTTAT  
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGCTCGGCACATAGTA  
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTAAGGGACAGAGCTTTACCTG  
GCAGTGATAAAGATGGGCTGTGGAGCTTGAAAAACCACTCTGTTTTCTTGCTCATACAG  
CAGCACATATTATCATACAGACAGAAATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAAA

## FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVLSIESEDEQKLIKFIENLLPSDGDWIGLRRREEKQSNSTACQDL  
YAWTDGSIQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPFMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAEGETELTPVLPEETQEEDAKKTFKESREAAALNLAYILIPSIPLLLLLV  
VTVVVCWWICRKRKRQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
 ATCCGACAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
 GTTTGCCTCCTGCAGCCTCAACCCGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
 GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGTGGCGTACTGCCTGCACC  
 AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
 CTGTGTAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCTCTCAAGCC  
 GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCAAGCTATTAGAGGTCCCACCCCAAACCTC  
 AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
 CAATACCATGAGACCACCTGAAGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT  
 GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAAGTATGTGAAGACATTCCCTTTC  
 TTTACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTG  
 GAGTCCACCCGTTGTTTGTCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT  
 CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA  
 GGCAGAGAACCAGAGGCCGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTG  
 AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT  
 GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAGCTGCCCATGCTGAAGAGATTG  
 CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGACATACTGCCAAGGAAGACAGG  
 GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
 CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
 TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGAACCACAAATGGCCACCGTTTGCT  
 GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA  
 TTACCAGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCTGGACATGT  
 TCTTGAATGCCATGTGAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA  
 ACTCAGGTGATGGAAGTTGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
 TTAAAATAAAGTGCCTTTATACAATG

## FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLKLKMKVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFCQKE  
GPIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD  
FFILLDNVAEQAHNLPSCPMLKRFFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

### **Signal sequence:**

amino acids 1-23

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

### **Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

### **Tyrosine kinase phosphorylation site.**

amino acids 280-288

### **N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

### **Amidation site.**

amino acids 216-220

### **Leucine zipper pattern.**

amino acids 10-32

### **Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTCTAGCTCATCACCTTTCACCTGCCTTGGTCTAGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAAGGACGTGGCTGTGTTGTGCGGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA  
GTCCACAGAGGGTGTCTAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCACTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG  
TGTGCCGCGAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAAACCCATCTGGCTGAGCCAGATGTCTGCTCAGGACGAGAAGCAACCCCTTCA  
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCTAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGCTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGGGTTTACGACTGCAACCCACAGGAAGA  
TGTGGCTGTCTATGCTCAGTGTAGCTGGGCATCATCTAATCTGTTGAGTGCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCTAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA  
CCACCTTTCTTATGTTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTTCTACACACACACACACACACACACACACACACACACACATA  
CACCATTGTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTTATTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPEAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC  
ENPESSFSFPVEGVR LADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKG VWSVCDNNGEKEQVVKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGTCTGTTCCGGCTGCCTGGG  
CGTCTTCGGCCTCTTCCGGCTGTCTGCAGTGGGTGCGCGGGAAGGCCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAAATGTGCAAAAGCTTCTTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGTGTGAGACTTTAATGGAGATTGTCTCACAAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGCCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGCGCCCATGGCCCAACTGTGTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLFLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVDRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGMKSI  
PFRSAYAASKHATQAFFDCLRAEMEYIEVTVISPGYIHTNLSVNAITADGSRYGVMDDTTT  
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVLYRLTAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17



# FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
 AAAAAAAAAACACACCAACCGCTCGCAGCCACAAAAGGATGAAATTTCTTCTGGACATCCTC  
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCTTCGTGAAGCTTTTATTCCTAA  
 GAGGAGAAAATCAGTACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA  
 GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
 CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTCATACCTTTGT  
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGTGGAAGGCAGAAATTG  
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGTCTACA  
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA  
 GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCTAGTGGCTTCGGCAG  
 CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
 TTTTATAAACTTTGACAGATGAACCTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
 TCTGTGTCTTAATTTCTGTAAACACTGGCTTCATCAAAATCCAAGTACAAGTTTGGGACCCA  
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
 ATTTTTATTCCATCTTCTATAGCTTTTTTAAACAACATTGGAAAGGATCCTTCTGAGCGTTT  
 CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAATGA  
 AAGCGCAATAAGACACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA  
 ATAGTGCCAGAATTTTAATGTTTGAACCTTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA  
 TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCATTGTCTTTAGCCAAAAGCTGATT  
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
 CCAAAATGACTTTATTTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
 AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTGT  
 ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAAACTTCAAGCTCTCTAAATAAAA  
 TGAAGGACTATATCTAGTGGTATTTTCAATGAATATCATGAACTCTCAATGGGTAGGTTTC  
 ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
 GCACAGGGAAGCTAGAGGTGGATACCGTGTGCAAGTATAAAGCATCACTGGGATTTAAG  
 GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
 AA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 58

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMI FIPSSIAFLTTLERILPERFLAVLKRRKISVKF DAVIGYKMQAQ

### Signal sequence:

amino acids 1-19

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

### Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

### N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC  
AGGGAGGAGCACCGACTGCGCCGACCCTGAGAGATGTTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGTCCTGTTGATGCCCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT  
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCTCCACCGTGAATAAGACTTACAACAGCAACCTCTTCTCTGGTTC  
TTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTTCATCCATGTTGGACTCTTTGGGAACATGGGCCTTATGTTGTACAAGTAACATGA  
CCTTGCGTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT  
AGCACGGGATTTATACAGTGCCTAATTTCAGTTTTTCCAGATATTTCTGAATATAAAAAATA  
ATGACTTTTATGTCACTGGGAGTCTTATGCAGGGAATATGTGCCAGCCATGTCACACCTC  
ATCCATTCCCTCAACCTGTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCTGTACCAAAATTGGCT  
TGTTGGATGAGAAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACAATC  
AGGAAGCAGAAGTGGTTTGAGGCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC  
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT  
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAA  
GCCATCCAGTGGGGAATCAGACTTTTAATGATGGAACATATAGTTGAAAAGTACTTGCAGAG  
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGG  
ATGGACTGGAAGGATCCAGGAATACAAGAAGGCAGAAAAAAGTTTGAAGATCTTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGCAAGCGGGTGACTTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAAATCGA  
TTCATTTATGGAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAGAGAACAT  
CAGAGGTTTTTCATTGCTGAAAAGAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAA  
TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAAATATCCTTGAAACCAAGTGAGC  
TTTTGTTTTTGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA  
AATTTTAGGGTCTTGAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATTGGATAAGAAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA  
TAGTTTTGGGGAAAGATCTCAAATGTATAAAGTCTTAGACAAAAGAATTCTTTGAAATA  
AAAAATATTATATATAAAAGTAAAAA

## FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGD SGQPLFLTPYIEAGKIQKGRELSL  
VGPFPG LNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVT SNMTLRDRDFPWTTT L SMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALI QF  
FQIFPEYKNNDYFVTGESYAGKYVPAIAHLIHS LNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAF EILDKLLDGLTSDPSYFQNV TG  
CSNYYNFLRCTEPEDQLYYVKFSLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVK PWLT  
EIMNNYKVL IYNGQLDIIVAAALTERSLMGMDWKGSQEYKKA EKKVWKIFKSDSEVAGYIRQ  
AGDFHQV IIRGGGHILPYDQPLRAFDMINRFIYKGWD P YVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

# FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCAGTCTTGTGGCTACAACAT  
TTTTCCCTTTCCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAAGCTCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCACTTGACCTGGAGAGC  
CTGGGGGAGGGCTGCTTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTTAATATCAAATTGACTGGCTGGG  
TGAACCTTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTTGTAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTTCCCTGAACATTTCTTAAGAGGGAGAAAGTATGTTAAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAAGGATGGGGACCTGGGT  
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACCTCTGCCTTGTGTTTT  
GCAGAATCATGTGAGGGCCAAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCGCCCTCTCAGCATGGAAACAGAGGCAGCCCTGGCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGCTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC  
ATGCTCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGACCTCTCAACCTTGACCGT  
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT  
CATCTGTGACTACTCTGAGAACCGCCTGTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA  
AGCTGTGCGGGCTGGATGACCTCTTATCCTGGTGGAGCCATCCCAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCAGCCCTGTCCA  
GCCGAAGCTGCCCGAGACCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT  
CTTCTACATCTACGGCTTTGTAGTGGGGCTTTGTCTACTTTCTACTGTCCAGCCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGGC  
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC  
CGGGGTGGAATACCGCCCTCTGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCCC  
AGGCCTTCAATATCACAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG  
CAGTATCACCAACCCCGCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACT  
GCAGATCAAGGAGCGCCTGCAGTCTGTCTACCAGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCCAGTGCACGAAGGCCCTGTCCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACCAAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC  
CAGAGGGGACCGCATGACCTCTGTGGCCTCTACGTTTACAACGGCTACAGCGTGGTTTTG  
TGGGAGCTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC  
ATTCACTCTCAGCAAGAGTCCCTCTTGAAGGTAGTATTGGTGGAGATTGAGTATTAATGATG  
GCACTTTATTTCTTGGGAACAAAGGTGAATGGGGAGGTAAAGAGGGTTAATTTGTG  
ACTTAGCTTCTAGCTACTTCTCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTTCCCAACTTTAAGAAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPNGYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQFWP  
RALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL  
YQGVCKLLRLDDLFIIVPEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPRDPESAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGASGGFVYFL  
TVQPETPEGVAINAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAAQAFNITSQDDVLFALFISKGQKQYHHPDDSAFCAPPIRAINLQIKERLQSCYQGEEN  
LELNWLLGKDVQCTKAPVPIDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTGSKGLKKVRVYEFRCNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGGCTGAGTGCAGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCGATGACCA  
CGTGGAGCTCCCGCGGAGGCGCGGCCGACGCTGGGACTCCTGCTGGTTCGCTTTGGGCTTCTTGGTCTCC  
CGAGGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGGCTCGAGAGCCAGGGGCTGA  
ACTTCATGCTGGAGGATTTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTTTCCGCTGGCCAGGGAGTACT  
GGAGGAGACCGCTCTGAAGATGAAGGCTGTGGCTTGAACACCTCACCACCTATGTTCCGTGGAACTCGCATG  
AGCCAGAAAGAGGCAATTTGACTTCTCTGGGAACCTGGAGCTGGAGGCTTCGTCTGTATGGCCGAGAGATCG  
GGCTTGGGTGATTCTCGCTCCAGGCCCTTACATCTGACGTGAGATGGACCTCGGGGGCTTGGCCAGCTGGCTAC  
TCCAGAGCCCTGGCATGGGCTGAGGACAACTTACAGGGCTTCCACGGAAGCATGGACCTTTATTTTGAACACC  
TGATGTCCAGGGTGTGGCATCTCAGTACAAAGCGTGGGGACCTATCATTCGCGTGCAGGTGGAGAGTGAATATG  
GTTCTCTAATAAAGACCCCGCATACATGCCCTACGTCAGGAAGGCATGGAGGACCGTGGCATTTGGGAACCTGC  
TCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTTGCCAGGGATCTTGGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGCACCACTTTCTCTTCAACGTCAGGGGACTCAGCCCAAGATGGTGATGGAGT  
ACTGGACGGGTGGTTTGACTCGTGGGGAGGCCCTCACATATCTTGGATTCTTCTGAGGTTTGAACACCGTGT  
CTGCCATTGTGGAGCGCGGCTCCTCCATCAACCTCTACATGTTCCAGGAGGCACCACTTTGGCTTCATGAATG  
GAGCCATGCACCTCCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG  
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC  
TGGGGGAGCCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTCT  
TCGGGTACATTCTCTATGAGACCGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG  
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAG  
GCTTAAATGGAAATCTCTATCTGAATGATTACCCCTGAAAAAATCTCAGAATCTATAGCTCGGATATGAAGAA  
GCTTCTTTTTCAGAGGTTGGGCTGGACAAATGGNGTTCCCTCCAGAAAACCCACATTAACCTGCTTTCTTTGG  
GTAGCTTGTGCATCAGCTCCACGCTTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA  
TCAATGGCCGAACCTTGGGTTACTGGAACATTGGACCCAGAAGACGCTTTACCTCCAGGTCCCTGGTTGA  
CGAGGGAAATCAACAGGTCATCGTTTGGAGGAGACGATGGCGGGCCCTGCATTACAGTTCACGGAACCCCC  
ACCTGGGCGGACCCAGCTATCAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCAGTGGGAGTGCAGGCTC  
CTCTTGACCTGAAGCCTGTGGCTCTGCTGCCCAACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGG  
ACTGGGGGCTCAGCTCGCCCTGTCTCAGCTCAAAACCTTAAGCCTGCAGGGAATGGGATGGCTTGGGCC  
TGCTTTTGTATGATAGGCTTTCTTACAGCCCTGCTCTTGTGCCGAGGCTGTCCGGGCTGTCTTAGGGTGGGAGC  
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAGGTGCTGAACGTCGCCCTTGACCCGGAACCTCACAGCC  
TSGCAGCATCTGCTGACCTCAGGCTGTCTTTTGTGCTTCTTGGAGGCTTGGCCATCCCTCATGGCCCAT  
TTTATCCCGAATCTTGGTGTGTCTCAGGTGTAGAGGTTGGGAAGGGGCTTCTCACCTGAGCTGTCTTGT  
CTTCTTCAACAACCTTCTGAGCCTTCTTGGGATTTGGAAGGAACCTCGGCGTGAGAACAATGTGACTTCCCCCT  
TCCCCCTCCACTCTGCTGCTTCCACAGGCTGACAGGCTGGGCTGGAGAACAGAAATCCTCACCTGCTGCTTCC  
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCATGGCCCATGTCTGCA  
CATCCAGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCATGGCCCATGTCTGCACATCCAGGA  
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCATGGCCCATGTCTGCACATCCAGGAGGAGG  
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCAACCCCGACGCCGAACAGCAGGGGACAGAGCAGCCCTCTTC  
GAAGTGTGTCAAGTCCGACTTTAGGCTTGTCTGGGGCCAGCCCAACACCTGGTGGGGCTCACTGTCTCTGA  
GTTGCAATAAGCTATAACCTTGAATCAACA

## FIGURE 64

MTTWSLRRRPARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHYFRVPREYWRDRLKMKACGLNTLTYYVPWNLHEPERGKFDPSGNLDLEAFVIMA  
AEIGLVWVILRPGPYICSEMDLGGPLPSWLLQDPGMRLRRTYKGFTEAVDLYFDHLMRSRVVPLQ  
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLAT  
INLQSTHELQLLTFLFNVQGTQPKMVMMEYWTGWFDSWGPHNILDSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSI SGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYI IYE  
TSITSSGILSGHVHDRGQVFNVTVSIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSL SIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

### **Signal sequence:**

amino acids 1-27

### **Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

### **N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586



# FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGTCAAGACGCGAGGACCTTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGGTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCCTGGCCTTCGTTCCCTGCTGCTGCCGTCAAGCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTGCTTCGTAGTGGATAGGGGTATGACCGGTTTCTCCTAGACGGGGCCC  
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC  
CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTTATGTGCCCTGGAACATA  
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATGTCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCACTAGACAGGACCTTACATCTGTGACAG  
TGGGAGATGGGGGTCTCCCATCTCGTTGCTTCGAAAACTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCCTTGCCCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC  
CATGGCTTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTCCGTGCACTGCTAGG  
AGAAAGATCTTGCTCTTCCACACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACCTGTAGATTTTGGCCAGCTGACAACATGACCAAAATCTTTACCTGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAACCAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG  
AATGTTGCCGATAAGAAGGGACGCTTCTTCCGATTACTACAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGTCTTCGAGATGTCTATCAGCAAGT  
TCCAGGAAGTTCTTTGGGACCTTACCTCCCCGAGCCCCAAGTATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTCTTGCCCGTGGGCCCAT  
TCATTCAATCTTGCCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC  
GAACCTATATGACCCATACCATTTTTGAGCCAAACACATTCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCTTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTTGGAGCGAAATATGAG  
AGACAAACTATTTTGAACGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATCTG  
GGGCAAAACAATCTTACCCAGTGGATGATGTTCCCTCTGAAAAATGATAACCTTGTGAAGTG  
GTGGTTTCCCTCCAGTTGCCCCAAATGGCCATATCTCAAGCTCCTTCTGGCCCCACATTCT  
ACTCCAAACACTTCCAAATTTTAGGCTCAGTTGGGGACACATTTCTATATCACTTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGTACTGGACAAAGCAGGGGCC  
ACAACAGACCCCTCTACGTGCCAAGATTCTGCTGTTTCTTAGGGGAGCCCTCAAACAAATTA  
CATTGCTGGAAGTAGAAGATGTACCTCTCCAGCCCCAAGTCCAAATTTTGGATAAGCCCTATC  
CTCAATAGCACTAGTACTTTGACAGGACACATATCAATTCCTTTTACAGTGATACACTGAG  
TGCTCTGAAACCAATGGAGTTAAGTGGGCATTGAAAGGTAGGCCGGGCTGTTGCTGCTGCTG  
CTGTAATCCCGACCTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA  
CCAGCTTGCCCAACATGGTGAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGGCGTG  
ATGGTGGGCACCTTAATCCCGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGACGTGAGTGGAGGTTGTACCACTGCACCTCCAGCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAAAA

## FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRHDFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF  
TLLRKYEPHGPLVNSEYTTGWLDYWGQNHSTRSVSAVTKGLNMLKLGASVNMYPFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFAIRDVISKFQEVPLGLPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGFIHSILPMTFEAVKQDHGFMLYRTYMTHTIPEPTFFWVFN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGLKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDFTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTTGAACACGCTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT  
CTTTGCAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCAGATGTCAAAAACGATTTT  
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT  
CTTGTCAGAAGTTAGTGAAAAATAAECTTAGGGAAATTAGTTTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTTACAGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTTCATG  
CTGTGCGGGGTGCCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCTGGGTGTAATTTGCTCAAAAA  
CCTTCGAGAGTTGTACTTTAATAGGCAATTTGAACCTCGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCAGTGAAGAGCAATTTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATATAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA  
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAAGCTGGAT  
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAAAGACT  
GACTTGTTTAAAAATTATGGCATAACAAAATTGTTACTATTCTCTCCCTCTATTACCCATGTCA  
AAAACCTGGAGTCACTTTATTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCGAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACCTG  
CTTGGACCGCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTG  
TGGAAGATCACCTTTTTGATACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCTTTTGCAAGTTGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AATTCCTAGATTGCAAGTGTCTCAGTACAAGTTATTACAAGATAATGCAATTTTAGGAGTAG  
ATACATCTTTTAAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTAGGGTTTTAAGTCATTCAATTTCCAAATCATTTTTTTTTTCTTTTGGGG  
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTTAAATGTTTGTAACTTGGAT  
GCTGCCGCTACTGAATGTTTACAAATGCTTGCCTGCTAAAGTAAATGATTAAATGACATT  
TTCTTACTAAAAAAAAAAAAAAAAA

## FIGURE 68

MAYMLKKLLISYISIIICVYGFICLYTLFWLFRIPLKEYSFEKVVREESSFSIDIPDVKNDFAF  
LHMVDQYDQLYSKRFGVFLSEVSENKLRREISLNHEWTFEKLQRHISRNAQDKQELHLFMLS  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKKNLRELYLIGNLSENKMMIGLESRLRHLKILHVKSNTKVP  
ITDVAPHLTKLVIHNDGTLKLLVLSLKKMMNVAEELQNCCELERIPHAIFSLSNLQELDLKS  
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESYFSNNKLES  
KLRCLDVSNNNIMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKRLTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCRLDRLPAQLGQCRMLKKSGLVVEDHLFDLPLEVKEALNQDINIP  
FANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

# FIGURE 69

CCCACGCGTCGCGCCTTCTCTGGACTTTGCATTTCATTCTCTTTTCATTGACAACTGACTTTTTTATTCTT  
 TTTTTTCCATCTCTGGGCGAGCTTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT  
 CTGTGTTTTGGGGTTTTCTTCTCTCCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACACGTGG  
 GCTCAGTGTCTGTTGCTTCACTTATCTGCTAGGTACATCGAAGCTTTTGACCTCCATACAGTGATTATGCTCTGC  
 ATCGCTGTGTGATCTCTGGCGGCTTGCTCTGCTGATAGTTGTGCTGCTCTGCTTTACTTTCAAAATACACAAC  
 GCGCTAAAGAGCTGCAAGGAACCTGAAAGCTGTGGCTGTAAAAAATCAACAACCCAGACAGGTGTGGTGGGCGAAG  
 AACAGCCAGGCGCAAAACCATTTGCCACGGAGTCTTGTCTGCGCTGCGAGTGTGTGAAGGATATAGAATGTGTGCC  
 AGTTTTGATCTCCCTGCCACCTTGTCTGTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAAA  
 GCAGAGCCCTGAAGAGCTCAATGATGTCAATGAGGCCACCTGTTTTGTGATGTGCAGGACACGAAGAAAGGCACAG  
 CTCCTCCATGTTTTCATGGAATAAATTAATCTCAGTGCTGCTGGGAACCGAGTGTCTGGAGATCCCTACAGAGAGCTTC  
 CACTGGGGCGCAACCTTCCAGGAAGAGTGTGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACACAGTCA  
 CACAGCTGCTCTATTCTCACAAATCTACCCCTTGCGTGCGTGGAACTGACGCTTTCCCTGGAGGTGTCAGAAA  
 GCTGATGTAAACACAGAGCCTATAAAAGCTGTGCGTCTTAAAGCTGCCAGCGCTTGGCCAAATGGAGCTTGTA  
 AGAAGGCTCATGCCATTGACCTCTTAATCTCTCTCTGTTTGGCGAGCTGACAAATGGCGAGGCTGAAGGCAAT  
 GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCAACAAGGCATGATCTTGCCTCAATCCC  
 AGTGAGAACTGCACCTGGCAATAGAAAGACAGAAAAACAAAGCATCAGAAATTATCTTTCTCTATGTCCAGCTT  
 GATCCAGATGGAAGCTGTGAAAGTGAACCAATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCGCTCTGTAGGG  
 CAAGTCTGCAGTAAAAACGACTATGTTCTCTGATTTGAATCATCATCCAGTACATTGACGTTTCAATAGTTTACT  
 GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTAACTCTCTATGCCAACTGT  
 GGGCGTTTACCTGGATACCTTGGAGGATCCTTACCAGGCCCAATTAACCCAAAGCCGATCTGAGCTGGCTTAT  
 TGTGTGTGGCAGATACAAGTGGAGAAAGATTACAAGATAAACTAACTTTCAAAGGATTTTCTTAAGATAGAC  
 AAACAGTGCAAAATTTGATTTCTTGCCATCTATGATGGCCCTCCACCACTCTGGCGTGTGAGCAAGCTGTG  
 GGCCGTGTGACTCCCACCTTGAATCGTCACTCAAACTCTCTGACTGTGCTGTGCTCTACAGATTATGCAACTTCT  
 TACCGGGGATTTCTGCTTCTCAACCTCAATTTATGCAGAAAAACATCAACACTACATCTTTAACTTGGCTTCT  
 GACAGGATGAGAGTTATTATAAGCAAACTCTACCTAGAGGCTTTTAACTCTAAATGGGAATACTTGCAACTAAAA  
 GACCAACTTGCAGACCAAAATTTATCAAAATGTTGTGGAATTTTCTGCTCCTCTTAATGGATGTGGTCAATCAGA  
 AAGGTAGAAGTCACTCAATTTACTTACCAATATAATCACTTTCTGCATCCTCAACTTCTGAAAGTATCACC  
 CGTCAGAAACACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATCTACAGTGGAGATAATATACATAACA  
 GAAGATGATGTAATACAAAGTCAAAATGCACCTGGGCAATATAACACCGCATGGCTCTTTTGAATCCAATTCA  
 TTTGAAAGACTATATTGAATCACCATAATATGTGGATTTGAACCAAACTCTTTTGTTCAGGTTAGTCTGCAC  
 ACCTCAGATCCAAATTTGGTGGTGTCTTGTATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC  
 TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAACTGTGAAGGTGTATCCCTTATTTGGACATATGGGAGA  
 TTCCAGTTTAAATGCTTTAAATTTCTGAGAAGTATGAGCTCTGTGATCTGCAGTGTAAAGTTTGTATATGTGAT  
 AGCAGTGACCACAGTCTCGCTGCAATCAAGGTTGTGCTCCAGAAAGCAACGAGACATTTCTCATATAAATGG  
 AAAACAGATTCCATCATAGGACCATTTCTGCTGAAAAGGGATCGAAGTGAAGGCAATTCAGGATTTTCAGCAT  
 GAAACCATGCGGAAGAACTCCAAACCGAGCTTTCAACAGTGTGCATCTGTTTTCTTCTCATGTTTCTAGCTCTG  
 AATGTGGTGTACTGTACGCAATCAAGTGTGGCATTTGTAAATCAACGGGACAGCTACAAATACCGAAGCTG  
 CAGAACTATTAACTAACAGGTCCAACCTTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCTG  
 GGCTACACATATTATGAATAAATGAGGAAGGGCTGAAAGTGACACACAGGCTGTGAAAAA

## FIGURE 70

MELVRRLLMPLTLLILSLAELTMAEAEAGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIIRIIIFSIVQLDDPDGSCSENIKVFDGTSSNGPLLGGVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFVYFFSPNISIPNCGGYLDLTLEGSFTSPNYPKHPPELAYCVWHIQV  
EKDYIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFVSPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQQLQIIIVKCEMGHNST  
VEIIYITEDDDVIQSNALGKYNTSMALFESNSFEKITLESPYYVDLNTLQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLI CDSSDHQSRCNQGCVSRSKRDISSYKWKTD SIIGPIRLKDRSASGNSGFQHETHA  
BETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQLQNY

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 571-586

### **N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### **Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

### **N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

# FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCGAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGC  
TGCTGCGCCGCGCGCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC  
CTGGACGCCCGCCAGCTGCCCCGCGTGGTTTGACCAAGGCCAAGTTCCGCATCTTCATCCACTG  
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGATTTGGCAAAGGAAA  
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCTCCTAGTTTCAAATATGAAGAT  
TTTGGACCACTATTTACAGCAAAATTTTTAATGCCAACAGTGGGCGAGATATTTTTCAGGC  
CTCTGGTGCCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTTACCTTTGGGGGG  
CAGAAATATTCTGGAACCTGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAAGGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGACTGTACTATTCCTTTTTTGA  
ATGGTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTTCATTCATTAAGCGGCAATTTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCCCGGATCAATACTGGAACAGCACAGGCTTTCTGGCCTGGTT  
ATATAATGAAAGCCGAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAGCATGTTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTGCCA  
CATAAATGGGAAAACATGCATGACAAATAGACAAACTGTCTGGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG  
GAGGAAATCTTTTGATGAATATTGGGGCCACACTAGATGGCACTTTCTGTAGTTTTTGAG  
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAAGTCAATGGAGAAGCTATTTATGAAACCTA  
TACCTGGCGATCCAGAAATGACACTGTACCCCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCCCTGGCCAT  
CCCCAAGCTATTTCTGGGGCAACAGAGGTGAACTACTGGGCATGGACAGCCACTTAACCTG  
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC  
CGTGAAAATGGGGCTGGGCTTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAAACTGGAATAAGAAAATTTTGGCAGTTGAGCCCTTTCCCTTTTCCCACTA  
AATTTTTCTTAAATACCCATGTAACCATTTTAACTCTCCAGTGCATTTGGCATTAAAGTC  
TCTTCACATTGATTTGTTCCATGTGTGACTCAGAGGTGAGAATTTTTTACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAAATTTTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGTCTAGTCAAT  
TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTTTGGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACCTGTAGGCAATAGTAAACAGTGGTATTTGTATATCGAAACATATGGAACATAGAGAAG  
GTACAGTAAAAATACTGTAATAAATGGTGCACCTGTATAGGCACTTACCACGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCCTAGGACATTA  
TTGAACATCTGCCAGAGCTTATAAACTGTATGCTTAGGCTACACTACATTTTATAAAAAAA  
GTTTTTCTTCTCAATTATAAATAAATAAGTGTACTGTAACTTTACAAACGTTTTTAATT  
TTTAAACCTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAACATAAACCTCATTGTGCAA  
ATGTAA

## FIGURE 72

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPWTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSEFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEFW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVPDVWYTSKPKKELVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKKGWALALTNI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295



# FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCAGATGGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCATTCCATCTGGACACAGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
TTCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTTGTGAGCAAAAAGGCCAACCAGC  
AGCTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA  
TGGATTCTGGTGCATCTCTAGGATTAGCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGATTGGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT  
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATTATCAACACTCA  
AACTGCAACACAAACACAGAATTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCT  
ACTCTACAATACCTGCCCCCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATCCACGG  
AGAAAAAATTGATTTGTGTGCACAGAAGTTTTTATGAAACTAGCACCATGTCTACAGAAAC  
TGAACCATTTGTTGAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTC  
CCACGGCTCTGTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC  
TATGTCAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAATGAT  
CGAAACCAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAGA  
AACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCCTGGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGTTTCTTTCATGCTCC  
TTACCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCTT  
GGTTCTTAACCTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGC  
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCCACGGCC  
TTTCTAGCTTGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAA  
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCCAGCTCAGAC  
CCTTCTCTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCGGTA  
AGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCGTGAAAGCCATGGAGATTTCATAAAGTGG  
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTGTAACACATTGAGTTGGA  
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCAGTCTGATATTTCTCT  
AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAATTA  
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTCTCA  
GTTTGTATTTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTGAGACTAATCTT  
ATTCAATTTCTCTAATATGGCAACATTATAACCTTAATTTATTTAATACATACCTAAGAAG  
TACATTTTCTTACCTCTATATACCAAGCACATTTTAAAGTGGCCATTAAACAATGTATCACTA  
GCCCTCCTTTTCCAACAAGAGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA  
AGCATTTAGAAAACCT

## FIGURE 74

MARCFSLVLLLSIWTRRLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAPFPTNKNQOKEMIETKVVKEEKANDSNPNESKKTDKNPEESKSP  
SKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGCGGTCTTGGCACCTCTAATGCTCTCGTGATATCGGTGCCGCGACTTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTGGCCCTGCTCTCTGCTGCCTTCTCTACTCGTGAGGAA  
ACTGCCGCGCTCTGCCACGGTCTGCCACCCCAACGCGAAGACGGTAACCCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCTGTATGTTTTCTAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT  
TCTTTTCTTCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCATAGTGTTCC  
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAAC TAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA  
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC  
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC  
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG  
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCAACCACAGTGTGAGA  
TGGGGAAAACAAGAAGGATAAA TAAGATCCTCACTTGGCAGTGCTTCTCTCTCTGCAATT  
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTCCCTTTGG  
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTGAG  
GCACCTACAGGAAGGCCTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC  
AGCTATTGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCTTCTTAG  
TTGACCTGCACAGCTTGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTTCCCCAAGGACTCTTGCTTCCCTTAAGCCCTCTGGCTTCGTTTATGGTC  
TTCATTAAAGTATAAGCCTAACTTTGTGCTAGTCTTAAGGAGAAACCTTTAACCAACAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC  
TAACCTCTGACATACTCCCAACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT  
TCCTTTTG

## FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHGIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTQQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

[illegible]

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVIAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRLHRYDVFCFATALKGRVYYLEHPEKLTLTAEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPPVHPPNCGPPEPGVRSFGFPDPQSRLYGVCYRQH

### **Signal sequence:**

amino acids 1-17

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

### **Tyrosine kinase phosphorylation site.**

amino acids 137-145

### **N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

[illegible]

## FIGURE 80

MMWRPVSLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTRDRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 140-144

### **Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

### **N-myristoylation site.**

amino acids 263-269, 311-317

### **Endoplasmic reticulum targeting sequence.**

amino acids 325-330



# FIGURE 81

GGGGCCTTGCCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
 CGGGCGGGCGCGGGTGCAGAGGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTCGCTCCCAG  
 CCTGCTGTGTCGTGTTTGGCGCCCCGCCCTCCCGCGGTGCGGGGTTGCACACCGATCCTG  
 GGCTTCGCTCGATTTCGCCGCCAGGGCGCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
 CGGGTCGTCTGTGTCCTCTCTCTCTGCGCCGCGCCGGGGATCCGAAGGGTGCGGGGCTCT  
 GAGGAGGTGACGCGGGGGCTCCCGCACCTGGCCTTGCCCGCATTCTCCCTCTCTCCCAG  
 GTGTGAGCAGCCTATCAGTCACCAATGTCCGCAGCCTGGATCCCGGCTCTCGGCCCTCGGTGTG  
 TGTCTGCTGCTGTGCGGGGGCGGGGAGCGAGGGAGCCGCTCCATTGCTATCACATG  
 TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCCAGGGGGCTGCC  
 CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC  
 TGGTCGAGAAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT  
 GGTCTGCTCTTTACAGTAATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
 GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCGAGAAAGAAAAGTGG  
 CAATAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAGCTTAAATATTGGGCAGC  
 GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTGGGAATTGGAACA  
 GAAGGACCACATGTGGGCCTTGTTCAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA  
 AAACCTTTACATCAGCCAAAGATGTTTGTGTGGCCATAAAGGAAGTAGGTTTTCAGAGGGGGTA  
 ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATCTTTCACGGTAGATGCTGGA  
 GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTGGCCCTCTGATGACAT  
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA  
 AGCCTATCTCTGAAGAACTGGGGATGGTTCCAGGATGTACATTTTGTGACAAGGCTGTCTGT  
 CGGAATAATGGCTTCTTCTTACCACATGCCCACTGGTTTGGCACCACAAAATACGTAAA  
 GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
 CAGTGAACATTGCCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC  
 ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAATCTCGGACATTGGTGCCAAGAT  
 AGCTGCTGTACAGTTTACTTTATGATCAGCGCACGGAGTTCACTTCTACTGACTATAGCACCA  
 AAGAGAATGTCTAGCTGTCTACAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT  
 GATGCCATTTCTTCACTGTGTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAAGAA  
 CTTCTAGTAATTGTACAGATGGGCAGTCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
 CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
 AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCAAGAGAGATTACAGGATT  
 AGAACCAATTGTTTCTGATGTCTACAGAGGCATTTGTAGAGATTCTTAGAATCCAGCAAT  
AATGGTAACATTTTGACAACCTGAAAGAAAAAGTACAAGGGATCCAGTGTGTAAATTGTATT  
 CTCATAACTTGAATGCTTTAGCATACTAGAATCAGATACAAAATATTAAGTATGTCAAC  
 AGCCATTTAGGCAAAATAGCACTCCTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT  
 ACTTTGTTAAAAACACTCTGAGGCCTTCAATATCATGGCTCTTAGAAGCTCAGGAAGAGGA  
 GATAATGTGGATTAAAGCTTAAAGTCTTAAGAGTCTTAACCATGCCTACTAAATGTACAGATATGCAA  
 TTCCATAGCTCAATAAAGAAATCTGATACCTAGACCAAAAAAAAAA

## **FIGURE 82**

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRRGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNI AFLI  
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRES PNKNFLVIVTDGQSYDDVQGPAAAHAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

### **Signal sequence:**

amino acids 1-24

### **N-glycosylation site.**

amino acids 100-104, 221-225

### **Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

### **N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

### **Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCC  
GGCGGCCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGGCCCGCAGCGCAACTCGGTCCAGTCG  
GGCGGCGCGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCCACCCGTGTGCTGCTGC  
TGCTGGCGGCGCGGCTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGTCCAGTC  
AAGCCCGGCCGCTCTCAGTACCCGACGAGGAGGAGCCACCTCAATGAGATGTTCCGCGA  
GGTTGAGGAAGTGTGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG  
CAGAAGAAGCTGTGCTTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT  
CACAAATGAGACCAACACAGACAGAAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACACAGAGCTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGAGAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC  
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT  
CTGCACCCGGACAGTGTGTGTGGAGACAGCTGTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCGGGGAGCAATGGGACCATCTGTGACAAACGAGGAGCTGCCAGCCGGGGCTG  
TGCTGTGCCCTTCCAGAGAGGCTGTGTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA  
GCTTTGCCATGACCCCGCAGCGGCTTCTGGACCTCATCACTGGGAGCTAGAGCCTGATG  
GAGCCTTGACCGATGCCCTTGTGCCAGTGCCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTTCTGTGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC  
CAGAGAGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCGCT  
GCACCTGTGGGAGGGGAAGAGATTTAGATCTGGACAGGCTGTGGGTAGATGTGCAATAGAA  
ATAGCTAATTTATTTCCAGGTGTGTGCTTAGCGTGGGCTGACCAAGGCTTTCCTTACA  
TCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCAATTTGTTACG  
TCCCCAGGCTGTCTCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGACGGGTTAAAC  
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTGGCTCTACCAAGTTGGCAG  
ACAGCCGTTTGTCTACATGGCTTGATAATTGTTTGGGGGAGGAGATGGAACCAATGTGG  
AGTCTCCCTCTGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCCTGCTTTGCAACATCAA  
CCTGGCAAAAATGCAACAAATGAATTTCCACGAGTCTTTCCATGGGCATAGGTAAGCTG  
TGCCTTCACTGTGTGCAGATGAAATGTTCTGTTCACCCGCAATACATGTGTTTATTCATCC  
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGCGAGCATTTTCATATCCAAGATCAATTC  
CCTCTCTCAGCACAGCCTGGGGAGGGGTCATTGTTCTCTCTCCTCCTCAGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAAGCAGTGTTCAT  
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACAGCCTTGGTGCCACCAA  
AAGTGTCTCCCAAAAGGAGGAATGGGATTTTTCTGAGGCATGCACATGGAATTAAG  
GTCAAATAATTCTCACATCCCTTAAAGTAACTACTGTAGGAACAGCAGTGTCTCAC  
AGTGTGGGCGAGCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT  
TGCATTAGTAACTTTGAAGGTATATGACTGAGCGTAGCATACAGGTTAACTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAATGATGTTTTCAAGTGTCA  
TGAAGCTGTTGCCACCATGTATTATCATCGAGTCTTAAAGTTTAAAGTTGCACATGATTGTA  
TAAGCATGCTTCTTTGAGTTTTAAATATGTATAAACATAAGTTGCATTTAGAAATCAAGC  
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEAAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTR DSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLLCAAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

# FIGURE 85

AAGGAGGCTGGGAGGAAGAGGTTAGAGAACCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTTTCAGCCCACTCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACATACA  
CACACATACACCTTCTCTCTCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCTATAGAAAAGGACAC  
TAAGGCTTAAGGACAGGCTGGCCATTACCTTGCAGCTCTTTGGCTTGTGTAGTCAAAAAAATAGCCAGGAGTGGGAGG  
CCAGGACCGGTGACTCACACTGTAATCCAGCACTTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG  
TTCGAGACCAAGCTGGCCCACTGGAGAAACCCCACTCTACTAAAAATACAAAAATAGCCAGGAGTGGGTGGC  
AGGTGGCTGTAAATCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGTTGAATCCAGGAGGCGGAGGATCGAGT  
CAGCTGAGTGACCGCTGCACTCAGGCTGGGTGACAGAATGAGACTCTGTCTCAAAACAAACAAACAGGAGGAA  
GGGATAGATACTGCTTCTCTGCAACTCTCTTAACTCTGCATCTCTTCTTCTCAGGAGTGGCCCTGATGGGAGCTG  
GCAATGCTAGCAGGCTCCGAGGACAGGAAAGAGGATATTGAGGAGGGCAAGAAAGTGCAGCCCTGACGCCCG  
GTGTAGATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTTGCTGACCTTACCCTGCAAAAAACAA  
AAGAGCAGGACTCCAGACTCTCTTTGTAATGGTCCCTGCCCTGCACTGCTGAGCTCCACCTATGGGCTTCTGCTGGCC  
ACTCTGTAGCTTGGGTGGCTGGTGCACCTGCCACTGTGCCGTGGTACCCTGGCATGTTCCTGGCCCCCTCA  
GTGTGGCTGGCAGATCCGGCCCTGGTATACGCCCCCGCTCGCTCTACCCGAGAGGTACCCTGTGGACTGCAATGA  
CCTATTCTCTGACGGCAGTCCCGCGCACTCCCGCGAGGACACACAGACCTGCTCTGACAGACACAGCATTTGT  
TGCGCGAGACTGTGATTTCCTCATGCTTCCGCCAGCTGTCTGAGCTGCACCTAGAGGAGAACCACTGCTCCCGCT  
GGAGGACCAACAGCTTTGCAGGCTGGCCAGCCCTACAGGAATCTATCTCAACCAACCAAGCTTACCCCGCTCG  
CCCCAGGGCTTTTCTGGCTCAGCAACTTGTGTGGCTGCACTCAACTCCCACTCTGAGGGCCATTGACAG  
CCGCTGGTTTGAATGCTGCCCACTTGGAGATCTCATGATTGGCGGCAACAGGTAGATGCCATCTGTGACAT  
GAACTTCCGGGCCCTGGCCAACTCGGTAGCCTGGTGGTGTAGCAGGATGAACCTTGGCGGAGACTCCGACTATGC  
CCTGGAGGGGCTGCAAGGCTGGAGGCTCTCTCTATGACAAACAGCTGGCCCGGCTGCCCGAGGCGGCACT  
GGAAAGGTGCCCGGGCTCAAGTTCCTAGACCTCAACAAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTTGC  
CAACATGCTGCACCTTAAGAGCTGGGACTGAACAACATGGAGGAGTGGTCTCCATCGACAAGTTTGCCTGT  
GAACCTCCCGAGCTCCAAGCTGGACATCAACAAATACCCAGGCTGTCTTATCTCACCCCCCGCTTCA  
CCACTGCCCGAGATGGAGACCTCATGCTCAACAAACAGCTCTCAGTGGCTTGACACAGGAGCGGTGGAGT  
CCTGCCCAACCTGCAGGAGGTAGGCTCCACGGCAACCCATCCGCTGTGACTGTGTATCCCGCTGGCCAGCATG  
CACGGGCAACCGCTGTGCTTCTCATCGACGGCAATCCACCTGTGTGGGAGCTCCGGAGCTCCAGGCGCTCC  
GGTCCGTGAGGTGCCCTTCAGTTCAGTGCACCTGCCATGACGGACACTGTTTGGCCCTCATCTCCCAAGAGCTTCCCCAG  
CCTCAGGTAGCTGAGTGGAGAGGACTGGTGTGCTTCCCGGCACTGGCCGAACCCGAACCCGAGATCTACTG  
GGTCACTCCAGCTGGGCTTCGACTGACACCTGCCATGACGGCAGGAGGTACCGGGTATCCCCGAGGGGACCT  
GGAGCTGCGGAGGGTGCAGCAGAAGAGGCGAGGCTATACACTGTGTGGCCAGAACCTGGTGGGGGCTGACAC  
TAAGACGGTGTAGTGTGGTGTGGGCTGTGCTCTCAGCAGGCAAGGACAGGAGGAGGAGGCTGGAGCTCG  
GGTGCAGGAGACCCACCTTATCAGACTCTGTATCTTGGGTCAACCCACCAACAGTGTCCCAACCACTCA  
CTGTGCTCAGTGCTCTCTCCCTCGGGGCCAGGGGCCACAGCTTGGCCCGCTGAGTGGGGATCCCTGAGGCTGT  
CAACATTACCCGCTCTCTCAGGCCACGGAGTACTGGGCTGCTGCAAGTGGCTTTGTGTGATGCCACACCA  
GTTGGCTTGTGTATGGGCTGAGCAACAAAGAGGCCACTTCTGCCACAGAGCTTAGGGGATCGTCTGGGCTCAT  
TGCCATCTGGCTCTGCTGCTCTTCTCTGTGAGCTGGGCTAGCGGCCCACTTGGCAGAGGCAACCCAGGAA  
GGGTGTGGTGGGAGGGCGGCTCTCCCTCAGCTGGGCTTCTGGGGCTGGAGTGGCCCTTGTGTGCGGGTGT  
GTCTGCTCCCTCTGCTCTGCTCTGGAATCCAGGGAGGAAGCTGCCAGATCTCAGAAGGGGAGCACTGTGGC  
ACCATTGTCTCAAAATCTTGAAGCTCAGCTGTCTCAGCAGTAGAGAAATCAGTACGACTCTTTTACCAAA  
AGAGAAGCAGCTTGGGCCAGTGCCTGCCAGGAAAGGACATGGACCACAGTGTGTGAGGCTTGGCAGCTGGG  
CAAGACAGCTGGGCTTGTGGGCTGGGGTGTCTCTGACGCTTGAAAAAGTGGCCCTTACCTCTTAGGCTCA  
CCTCTGCTGCCATCTCAGGAACATCTCCAAGGAACAGGAGGAGCTTGGCTAGAGGCTCTCTGCTCCCATCT  
CTCTCTGCGAGAGGCTCTCTGGGCTGGCTTGGCTGTGCCCTACCTGTGTGCGGGCTGACCCCTCTCTCTT  
CTCTTCTCTGATAGCTCTCAGTTGCTGTCTTGTGCTCTTGGGCAAGGGCTGAAGAGGCACTCCATCTCAC  
CTCGGGGGCTGACCTCAATGTGGGAGTGACCCAGCCAGCTGAAGGACATTTGGGAGAGGATGCCAGGAA  
CGCCTCATCTCAGCAGCTGGGCTGGCATTCGAAGCTGACTTTCTATAGCAATTTGTACTTTTGTGAGAA  
ATGTGTCACTCCCCAACCCGATTCACTCTTTCTCTGTTTGTAAAAAATAAAATAATAACAATAAA

AAAA

## FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLQLQSNISIVRVDQSELGYLANLTDLDSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSAFGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKFAVLNLP  
ELTKLDITNNPRLSFIHPRAFHHLFQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVFPREMTDCHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRITPAHAGRIRYVYEGTLELRRTVAEEAGLYT  
CVAQNLVGADTKTVSVVVGRALLQGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRGQATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLLLAAGLAHLGTGQPRKGVGRRRLPPAWAFWCWSAPSVRVV  
SAPLVLPWNPGPKLPRSEGETLLPPLSQNS

### Signal sequence:

amino acids 1-18

### Transmembrane domain:

amino acids 629-648

### N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

### Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

### Tyrosine kinase phosphorylation site.

amino acids 532-540

### N-myristoylation site.

amino acids 15-21, 493-499, 566-572

### Amidation site.

amino acids 470-474, 660-664, 692-696

## FIGURE 87

GCAGGCAAGAGCGCTGTTTGAGAAGGTGAAGAAAGTTCGACCCATCTGGAGGAGGGGGACATTTGTTGACCGCTCT  
CTACATCAGCGACAGCATCATCAAGGTGTCAAGTTCACTCTCATCTCACTGCTACACGCTCTCTACGTGCACAA  
CTCAAGTTCGACGTGGATCGAGCTGGGACATTGAGAGCGTACGCGGCTACCGCACTACCGCTCTCGCCACC  
CTCGGCCACATCTCTCAAGATCTCGGCGCTCTTCTACATCAGCTAGTACCTCTCTACGCGCTCATCTGCATGTA  
CAGCTGTGGTGATGTCACGGCGCTCCCTCAAGAAGTCTGTTTGAGTGCATCGTGAGGAGAGACAGCTACAG  
CGCATCCCGGACGCTGAAGAACCATTCGCCCTTCTATGCTGCACCTCATTTGACCAATACGACCGGCTCTACTCCAA  
GGCTTTCGCGCTCTTCTGTTGGAGGTGTAGTGAGAACAGCTGCGGACGCTGAACTTCAACAACGAGTGGAGCGCT  
GGACAGCTCTCGCGACGGGCTACCAAGAAAGCGCGAGGACAGCTGGAGTGCATCTGTTATGCTCTCAGTGGTCA  
CCCTGACAGCTGTGTTTGAATCTGGTGGAGCTGGAGAGTCTCAAGTGGAGGTGATCCCGGAGTGACATCCGCG  
CAGCATTCGCGGACGCTACGGGCTCTCAAGGAGCTGTGGCTCTACACACAGCGCGCAAGTGTGAAGCGCTCGCG  
GGCTTCTCTGCGGAGAACTCTGGGCGGCTGCACATCAAGTTCACCGATCAAGAGATTCGCGTGTGGATCTA  
TAGCTTGAAGACCTCGAGGAGGCTGCACCTGCAGCGGCACTGAGCGGGAGAACCGCTATCATGTCATCGA  
CGGGTCTCGGGAGCTCAAAACGCTCAAGGTGTGGCGCTCAAGAGCACTAAGCAAGCTGCCACAGGTGTCTGA  
AGATGTGGGCGTGCACCTGCAAGAGCTGTCCATCAACATAGAGGAGCAACCGTATCGTCTCAACAGCTCAA  
AAGATGCGCAACTGATGTAGCTGGAGCTGATCGCTGCAGCTGGAGCGCATCCCACTTCATCTTAGCTCT  
CCAAACCTCGCAGGAGATTTAGCTTCAAGAACCAACAACTCAAGCATCTCAGGAGATCATAGCTTCCAGCACT  
GCACGCGCTCACTGCTTCAAGTGTGGTACCAACATCGCTCATCCCCATCAGATCGGCAACTCAACAA  
CTTGGAGCGCTCTTCACTTCAACCGCAACAGTTCAGAGAGATCCCCACAGCTCTTCTATCTGCGCAGCTCGG  
CTRACGTGACCTCAGCAACAAACCTTCAAGTTCTCTCGTGCAGCATCGCTCTCTGAGAACTTCAAGAACT  
AGCCATCAAGCAGCAACCGGATCGAGAGCTCTCTCCGGAGCTCTCCAGTTCGGGAGCTCTGGGCGCTGCACCT  
GGCAACAAACCTGTCTGCATCTAGCTGCCCTCAGGTTGGGCGAGTGCACCAACTGAGCGAGTGCAGTCTCGGG  
CAACCGCTCGAGAGTGCCTGCTGTGAGGCTGGGCGAGTCCCACTGCTCAAGCGACGGCTGTGGTGTGGAGGA  
GGACCTTGAAGCATCTGCACATGCCAGTGGAGGAGCGGCTGTCGAGGCTGACAGAGCAGCGCTTGGAGGAG  
GCGGCGCCAGCAGCAGCAAGCAGGACCGGCTCCGCGCTCTCAGCGCCGAGGGGCGAGGCTAGCTCTCCAG  
AACTCTCCGGACAGCGCAGGACAGGCTCGCGCTTCTCCCTCTGAGATCACTGCTCCCCAGGCAAGTGTCTTGGAGGAG  
GGAGCATATCTGTGGGCTGGCGCTTCTTCTCCCTCTGAGATCACTGCTCCCCAGGCAAGTGTCTTGGAGGAG  
AGCAACTCTCAAGAGCGCATATTTGATATCACTCAGGTTCTCTCTGGAGCGGCTCTGCCCAAGGGCTGAG  
CTGCACACAGAGGCTCTGGGACCTCACTTTAGTTCTGTGATTTATTTTCTTCATCTCCCACTCTTCACT  
AGTATAGTTATATACATCCCAAGAAAGTTTCAGCCAGTGGAGGTTGTCAGGAAAGTGGGCTGCTTTTCCC  
TTGTCTTATTTAGCATGTGCGCGGCACTTTAAACCAACCTGGACTTCAGCAGAGTGTCTCGGGCGAACCAG  
CCATGGGACGGTCAACCCAGAGCTGCCGGGCTGGGCTCTCGGCTCGCGTCCAGGAGAGCGGCTCAGCTGGA  
AAGGCGAGGCTGAGGCTTGCCTCTCAGTTTGTGGGAGCTTTGATTTTGTGTTTTTTTGTTTTTTATTA  
AAACAACTTTTTTTTAAAAAAGAGTTTGAATAAGTAGGTTTGGGATTTAAAAAGAAAAAATAATAAAAA  
AAAAAGACATACCGCGAGTGTGTGGAGTCTCAGGCGAGGCTGGAGTTTCCCTTGAGCAAGAGCGCAGGACT  
TGAATCTGTGTTCTCTTCCCTGGGCGAGGTTGAGGTTCTTCGGAATCTGTTGTGACCTTGTGTCAGAGTT  
CTATTGTCTCTGGGAGGAGGAGTTTGTGTTGTTTGTGTTTTTGGGTTTTTGGTGTGTTGTTTCTTCTCC  
ATGTTCTCTGCGAGCACTATTCTTGCTGCTCTCGGCGAGGAGGATGTTCTGAGCTGCCAAGGAGGAGGAG  
ACTCGGTTTGGCTAATCCCGGAGTAACGGTGCTCATTGACACTCCCCTCTCTGCTCTGCTGCTCTCCA  
CGCACGTGCTTAAGGAGCAGAGAGGACCACTTCGCGCAGACTTTGTTTCCCACCTCTGCGGACAGTGGTGTG  
TCAGTGGCACCGCTTGCCTCAGCTGCTCTCAATCAGCCCTCTGCCACCTTGTGTCATGAGGAGCAGCACTA  
GAGGCTGTGTCGGGATGGGAGGCTCGCCCTGGGAGGCGAGGCTGGTTTCAAGCGCGGTTCCGCTCTGGGCG  
CTGGAGTGCACAGCCAGCTCGGCACCTGTGGTGAAGCGAACCTGTTTATGATCATCGGTTCCCACCTT  
AGAAGGCTCCCGGCTTAGATCAATCACTGGACATAGGCACTTTTGAAGTCTCTGTGTTAAGTATGTT  
CCATCGCTCTGTCGTCATTTGTGTTTTTCGCTGTGCTAGTGAATAATCTCAGAAATATGACACATG  
CCTCTGACAACTTAGAAGCAAAAACTGCTTCAATGTGGGTCTGAACCTGTAGACTCGGTCAAGTATCAATAAA  
ACTATATAACAGAAAAAATAAAAAA

## FIGURE 88

MRQTI IKVIK F I L I I C Y T V Y V H N I K F D V D C T V D I E S L T G Y R T Y R C A H P L A T L F K I L A S F Y I  
S L V I F Y G L I C M Y T L W W M L R R S L K K Y S F E S I R E E S S Y S D I P D V K N D F A F M L H L I D Q Y D P L Y S K  
R F A V F L S E V S E N K L R Q L N L N N E W T L D K L R Q R L T K N A Q D K L E L H L F M L S G I P D T V F D L V E L V  
L K L E L I P D V T I P P S I A Q L T G L K E L W L Y H T A A K I E A P A L A F L R E N L R A L H I K F T D I K E I P L W I  
Y S L K T L E E L H L T G N L S A E N N R Y I V I D G L R E L K R L K V L R L K S N L S K L P Q V V T D V G V H L Q K L S I  
N N E G T K L I V L N S L K K M A N L T E L E L I R C D L E R I P H S I F S L H N L Q E I D L K D N N L K T I E E I I S F Q  
H L H R L T C L K L W Y N H I A Y I P I Q I G N L T N L E R L Y L N R N K I E K I P T Q L F Y C R K L R Y L D L S H N N L T  
F L P A D I G L L Q N L Q N L A I T A N R I E T L P P E L F Q C R K L R A L H L G N N V L Q S L P S R V G E L T N L T Q I E  
L R G N R L E C L P V E L G E C P L L K R S G L V V E E D L F N T L P P E V K E R L W R A D K E Q A

### **Transmembrane domain:**

amino acids 51-75 (type II)

### **N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

### **Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

### **N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447



## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCGCTGAACGCAGGAGCTGTCAATTGACT  
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTCGGTTCAT  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGGAACTTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACACGGAAAACACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTGAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT  
TGCCCTGGGTGATTCCTGGATCTCCCTGTTGATTGGTGCTCTCCTGGGACCTTACCTGT  
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACTAAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGTGACGCG  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGCTCTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGGCTG  
GGTGGCGGAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT  
ACAGTGACCCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCTACAAGAACCTTGCTTCT  
TACTGGATTCTGAAAGCTGGTCAATATGGTTCCCTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCGGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGGAAATTATTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

## FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRTTWLQAASLLFVDNPNVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTPVFFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGLYRE  
ATELWGKAEMII EQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRHVRLQRDALS  
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMQQEAWVRKLKWEPELPKFSQLKWKALYSDPKSLETSAFVKS YKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGCGCCGTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCGCATCTGGGTGGAGAGGACGCCGAACCTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATG  
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCCTGCCATCTCCCCACACCCTCCAGGAAGTTGAGTCGCCATCATAAACA  
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG  
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG  
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG  
CTGATGGCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT  
TCTCTGGGCTCTCCCACTCCTGGGGCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTGTTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 92

MGARGALLLALLARAGLRKPESEQEAPLSGPCRRVITSRIVGGEDAELGRWPWQGSRLRLW  
DSHVCVSVLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSSGGPLACNKNG  
LWYQIGVVSWSVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

# FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
 CTTTGCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCCGAGCCCCGACCAGCGGAGACGC  
 TGCCCCCAGGCTGGGTGTCCCTGGGCGGTGCGGACCTGAGGAAGAGCTGAGTCTCACCTTT  
 GCGCTGAGACAGCAGAATGTGGAAGACTCTCGGAGCTGGTGCAGGCTGTGTGCGGATCCCG  
 CTCTCCTCAATACGAAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
 CACTGACCCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAAGTGCCATTCT  
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAGCAGAGCTGTGTCTCCC  
 TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTGTAAGGTCCCCAC  
 ATCCCTACCAGCTTCCACAGGCCCTTGGCCCCCATGTGGACTTTGTGGGGGAGTGACCCGT  
 TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGACTGTAGGCCCT  
 GCATCTGGGGTAACCCCTCTGTGATCCGTAAGCGATAACAATTGACCTACAAGACGTGG  
 GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCTGGAGCAGTATTTCCATGAC  
 TCAGACCTGGCTCAGTTTATGCGCCTCTTCGTTGGCAACTTTGCACATCAGGCATCAGTAGC  
 CCGTGTGGTTGGACAACAGGCCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCGAT  
 ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
 GGACAGGAGCCCTTCTCGAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
 GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA  
 ACAGTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCTCAGGTGACAGT  
 GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAAGTTCCGCCCTACCTTCCCTGCCCTCCAG  
 CCCCTATGTCAACACAGTGGGAGGCACATCCTTCCAGGAACCTTTCTCATCACAATGAAA  
 TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG  
 GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
 CAGTGGCCGTGCCATCCAGATGTGGCTGCATTTCTGATGGCTACTGGTGGTCAACCAAG  
 GAGTGGCTTCCATGGGTGTCCGGAACCTCGGCCCTACTCCAGTGTGGTGGGATCCTGTCT  
 TCCTTGATCAATGAGCAAGGATCCTTAGTGGCCGCCCCCTCTTGCTTTCTCAACCCAAG  
 GCTCTACCAGCAGCATGGGGCAGGTCTCTTGATGTAACCCGTGGCTGCCATGAGTCTGTCT  
 TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGTCTGGTCTGGCTGGGATCCTGTAACAGGC  
 TGGGGAACACCAACTTCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCTCTATC  
 AGGAGAGATGGCTTGTCCCTGCCCCTGAAGCTGGCAGTTGAGTCCCTTATTTCTGCCCTGTG  
 GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
 TGCTGTGAGCTTGACTTGAATCCCAACCTTACCATGCTCCATCATACTAGCATTTTTGTAATGCCCTCTCCCTCCGC  
 CCGCTCTTAGATTCTCAATAAGATGCTGTAACTAGCATTTTTGTAATGCCCTCTCCCTCCGC  
 ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAGGGTTGTATACAGACTCTGTGACTA  
 TTTCACTTGATATTATTTCCCAATTCACTGCAAGGAGACCTTACTGTACCCTTACTCT  
 TTTCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATG  
 GCCTTTCCATCATAGTTGGCCACTCCCTCTCTTACTTACTGCTCCAGGTCTTAACCTTCTG  
 ACTACTCTTGTCTCTCTCTCATCAATTTCTGCTTCTCATGGAATGCTGACCTTCATGTC  
 TCCATTTGTAGATTTTGTCTCTCTCAGTTTACTCATTGTCCCTGGAAACAATCACTGACA  
 TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA  
 TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGYKYLLENVADLVRPSPPLTLHTVQKWLAAAGAKCHSVITQDFLTCWL  
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTSPVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVSNRVPWPVSGTSASTPVFGGILSLINEHRILSG  
RPPLGLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSPGWDPVTGWGTPTSQLC

### **Signal sequence:**

amino acids 1-16

### **N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### **Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

### **Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### **N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

GGCGCGCGCTCTCTCCGGCGGCCACACCTGTCTAGCGCGCGAGCGAGCGCGGCCGGGCGGGCTGTCTCGGCGCGGAACAGTGTCTGGCATGGCGAGGGATTCCAGGGCTCCTCTTCTTCTCCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTGGCTGTCATACCGCTCCCTGTGCTCTTGCCCCAGTCTACCTCAATTTAGCCAAGCCAGACTTTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTTCATGTGGACCCCAAGTGTCTATAAGGGAACCTACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGGCAGCCGACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCCAACACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGAGGTTTCAGCATTTTGGGAAGGACTTCTCTGCTCAACTACCCTTTCTCAACATCAGTGAAAGTTATCCACGGGCTGCACCGGCACCCTGGTGGCAGAGAAGCATGTCCTCAGCATGCTGCCCATGCAATACAGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGCTTCCGCTGCTCCCAAGCCAAAGTTTAAAGATGGTGGTGTGAGGGGCAACGAGCTTCACTTCAGCCATGCCCGAGCAGATGAAATTTTCAGTGGATCGGGGTGAAACGCCACCTATGTGCCCAAGGGTTGGATCAAGGGCAATGCCAATGACATCGGCATCGGGTGAACGCCACCTATGTGCCCAAGGGTTGGATCAAGGGCAATGCCAATGATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTAAAAAGCCCCACAAGAGAAAAATTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTTCTCTGGTTATGACAATGACCGACCAAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGACCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGCGGCTCTGGGGTCTATGTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTCAGGGCACCAGTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTCAGAATCACTCTCTCAAAATATGCCCAGATTTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGGTGAGACAGAGTGTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGGCCAAATTGTTTTTTGTTCATTGGCGTGACACAGTGTGTGTGTGTGTGTGTGTGTGAAGTGTCTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTGGAANAATCGTTTGTGTATCATATCATATATCATTAAGCAGTTTTGAAGGCATACTTTTGCATAGAAATAAAAAAATACTGATTTGGGGCAATGAGGAATAATTGACAAATTAAGTTAATCTTCACGTTTTTGCAAACCTTGATTTTTTATTTTCATCTGAACCTGTTTTCAAAGATTATATTAATATTTGGCATACAAGAGATATGAAAAAATAAAAAA

## FIGURE 96

MAGIPGLLFLFLFLLCAVGVQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHC IHDGKTYVKG  
TQKLRVGFLLKPKFKDGGRGANDSTSAMPEQMKFQWIRVVRTHVPKGWIKGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFGDVKDETYDLLYQQCD  
AQPASGSGVYVRMWRKQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177



## FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCCAGCCATGGTGGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCCTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCTGGGTGGAGC  
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTGC  
CCCAACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCTTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGCAACAGGCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGAAGGGGTGCA  
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT  
AGGTATTTGTAACCTGCCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTAT  
CTCAAAAAAAAAA

## FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
M V V S G A P P A L G G G C L G T F T S L L L L A S T A I L N A A R I P V P P A C G K P Q Q L N R V V G G E D S T D S E W P  
W I V S I Q K N G T H H C A G S L L T S R W V I T A A H C F K D N L N K P Y L F S V L L G A W Q L G N P G S R S Q K V G V A  
W V E P H P V Y S W K E G A C A D I A L V R L E R S I Q F S E R V L P I C L P D A S I H L P P N T H C W I S G W G S I Q D G  
V P L P H P Q T L Q K L K V P I I D S E V C S H L Y W R G A G Q Q F I T E D M L C A G Y L E G E R D A C L G D S G G P L M C  
Q V D G A W L L A G I I S W G E G C A E R N R P G V Y I S L S A H R S W V E K I V Q G V Q L R G R A Q G G G A L R A P S Q G  
S G A A A R S

### **Signal sequence:**

amino acids 1-32

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCCGTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCCTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC  
AACAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCCGCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGTAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAAGTGAAGGCCCATCCTTCCGGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAACCCAGGCC  
CCAATTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC  
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA  
CCTTCCCAAATCGACCCATGTTCTTATCCCAAATCAGCAGACAAAGTGACAGACAAAAACA  
AAAGTGCCCTCTAGGAGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG  
GGAACCTCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCTTCCAGTG  
AGGTCTTGCCCTCAGTTTTCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCTCCAGTCCCTGCCCAATTTCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA  
AGCCTAGCGTTGTGTCAAGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA  
CTACTGCTCCTGCCCTCCTCTGGTGTGGCTGGAATCTCTGAATGGGATACCACTCAAAGGG  
TGAAGAGGTGAGCTGTCTCCTGTCTCTTCCCCACCCTGTCCCCAGCCCCATAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCC  
ATCTTGAGGCACAAGGCCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCTGGGGTGGGAGGATTTGAGGGAGCT  
CACTGCCTACCTGGCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG  
TGAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC  
TTGAGTGGGGGAGGCAGGACGAGGGAAGGAAAGTAACCTCTGACTCTCAATAAAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLLVATGPGVGTDEEKRLMVELHNLRYAQVSP TASDMLHMRWDEE  
LAAFAKAYARQCVWGHNGKRGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVWAKTERIGCGSHFCEKLGQVEETNIELLVNENYEPGPNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSPRATEASDSRKMGTTPSSSLATGIPAFVLVTEV  
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLLLPPLVLAGIF

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

### **Glycosaminoglycan attachment site.**

amino acids 439-443

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

### **N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

### **Amidation site.**

amino acids 82-86, 172-176

### **Peroxidases proximal heme-ligand signature.**

amino acids 287-298

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

# FIGURE 101

GTAACTGAAGTCAGGCTTTTCATTGGGAAAGCCCCCTCAACAGAATTCGGTCAATTCCTCAAGTTATGGTGGACGT  
 ACTTCCTGTTGTTCTCCCTCTGCTTGGCTTTTTCACATTAGCAGACCGGACTTAAGTCACACACGATTATCTTTCAT  
 CAAGGCAAGTCCCATGAGCCACCTTCAAAGCCTTCGGAAGTGAACCTGAACACAAATGAATTTGGAGACCATTC  
 AAATCTGGGAGCAGCTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTTGAAATATCTCCCTGA  
 ACATCTGAAAGAGTTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCAACAATATTTAGAGCTTCAAAGCTGCATT  
 TCCAGCCCTCAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTTATTTGACAA  
 TTGGGCCAACACACTCCTTGTGTAAAGCTGAACAGGACCGAATCTCAGCTATCCCAACCAAGATGTTTAAACT  
 GCCCAACTGCAACATCTCGAATTTGAACCGGAACAAGATTAATAATGTAGATGGAATGACATTCCAAGCCCTTGG  
 TGCTCTGAAGTCTCTGAAATGCAAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTGGGGGCTTGAGCAA  
 CATGGAAATTTTGAGCTGGAGCCATAACAACCTTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGTATGCT  
 GCAGGAATCTCATCTCAGCCAAATGGCATCAACAGGATCAGCCCTGAGTCTCGGGAGTTCTGCCAGAAAGCTCAG  
 TGAGCTGGACCTTAATCTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTCTGGCCCTAAGCTTACTAATAAT  
 ACTGCACATTGGGAACAACAGAGTCAGCTACATTTGCTGATTGTGCCTTCGGGGGCTTCCAGTTTAAAGACTTT  
 GGATCTGAAGAACAAATGAAATTTCTCGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAG  
 GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCCTTCACTGGTTGGATGCATTGGAGCA  
 TCTAGACCTGAGTGACACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCACAACTT  
 GCATTTAAATACATCAAGCTTTTGTGCGATTGCCAGCTAAATGGCTCCCAAGCTGGGTGGGCGGAAACAACCTT  
 TCAGAGCTTTGTAAATGCGATTTGTGCCCATCTCAGCTGTCTAAAGGAAGAAAGCATTTTGTCTGTAGCCCTGAG  
 TGCGTTTGTGTGTGATGATTTTTCCAAACCCAGATCACGGTTGAGCAGGAAACACAGTCGGCAATTAAGCCCTG  
 CAATTTGAGTTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTTCCCAATGACTTTTGGCTGGAAAAAGACAATGA  
 ACTACTGCATGATGCTGAAATGGAAAAATTTATGCACACTCCGGGCCCAAGGTGGCGAGGTGATGGGATATACCA  
 CATCTTCCGGCTGCCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCCAATCACTTTGGTTT  
 ATCTCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAAAGCCCCATGGATCTCCACT  
 CCGAGCTGGGGCATGGCAGCTTGGAGTGTGCTGTGTGGGGCACCAGCCCCCAGATAGCTTGGCAGGAAGGA  
 TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGT  
 GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGACAGGAAGTATTTGACCAATGC  
 AACTCTGACTGTCTAGAAACACCATCATTTTGGGGCCTGTTGGACCGAACTGTAACCAAGGGAGAAACAGC  
 CGTCTACAGTGCTATGCTGGAGGAAGCCCTCCCTTAACTGAAGTGAACAGATGATAGCCCATTTGGTGGT  
 AACCGAGGCACTTTTTTGGCAGGCAATCAGCTTCTGATTATTGTGGACTGAGATGCTAGTGTGCTGGGAA  
 ATACACATGTGAGATGCTTAACACCTTGGCACTGAGAGAGGAAAGCTGGCCCTCAGTGTGATCCCCACTCCAAC  
 CTGCGACTCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCACTGTGGGTGTGCTGATCATAGC  
 CGTGGTTTGTGTGTGGTGGGACGCTCATCTGTGTGGTGGTCTATATACACACAGGCGGAGGAATGAAAG  
 TTGCAGCATTAACACACAGATGAGACCACTTGCAGCAGATATTCCTAGTTATTGTCTATCTCAGGGAACGTT  
 AGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGAAGGCCACCACAGTTTGTACATCTCAGGTGCTGG  
 ATTTTTTCTACCAACAAGATGACAGTAGTGGGACCTGCCATATTGACAAATAGCAGTAGAAGCTGATGTGGAGCTG  
 CACAGATCTGTTCTTTGTCCGTTTGGGATCCACAGGCCCTATGATTGAAGGGAAATGTGTATGGCTCAGA  
 TCCTTTTGAACATATCATACAGTTGCGAGTCTGACCCCAAGAACAGTTTAAATGGCACTATGAGCCCGATTA  
 CATAAGAAAGAAAGGAGTACCCATGTTCTCATCTTCAGAAAGATCTCGGAACGGAGCTTCAGTAATATATC  
 GTGGCCCTCACAATGTGAGGAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTTGAATGAAATCTGTG  
 TACTAAACAAGTCCCTTAGATTATTAGTGAACATCAGAGCCAGCGTCCGTTGCTCAGATTAATCTTTATGTTG  
 TACCTTTGAAAAGCTCTCAGAGACTCTCACCTTAGTGCTTATCAAGCTTTGGACAGCCATCAGATTGTGAGCC  
 AAGAGCTTTTATTGTAAGGCTCATCTTCCAGACTTGGACTCTGGGTGAGGAGAGATGGGAAAGAAAGGAC  
 AGATTTTTCAGGAAGAAATCACAATTTGTAACCTTTAAACAGACTTGAAGAACTCAGGACTCCAATTTTCACT  
 TTATGACTTGGACACATAGACTGAATGAGACAAAGGAAAGCTTAACTACTACTCACTCAAGTGAATTTTATTTA  
 AAAGAGAGAGATCTTATGTTTAAATGGAGTTATGAATTTTAAAGAGTAAAGATGCTTTTATTTATACAGAT  
 GAACCAAAATACAAAAGATTTATGAAAAATTTTATCTAGGAAATGATGCTCATATAAGAACTCTTTTAACTA  
 TTTTAACTTTGTTTATGTCAAAAAGATATCTTACGTAAATTAATGATATAAATCATGATTATTTTAACTA  
 TTATAATGCCAGATTCTTTTATGAAAAATGAGTTACTAAAGCATTTTAAATAATCTGCCTTGTACCATTTT  
 TTAATAGAAAGTTACTTCATTATATTTTGCACATTATATTTAAATAAATGTGCTCAATTTGA

## FIGURE 102

MVDVLLLFSLCLLFHISRDPDLSHNRLSFKASSMSHLQSLREVKLNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFALQLKYLNLNSNRVTSMEP  
GYFDNLANLTLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRRNKIKNV DGLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEILQLDHNNTL TEITKGWLYGLLMLQELHLSQNA INRISPD AWE  
FCQKLS ELDLTFNHL SRLDDSSFLGLSLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITTKAFTGLDALEHLDSLDAIMSLQGNFASQ  
MKKLQQLHLNTSSLLCDCLKWL PQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGH PAPQIAWQKDGDTFFAARERRMHVMPEDDVFFIVDVKIEDIGVYSTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER  
HFFAAGNQLLII VDSDVSDAGKYTCEMSNTLGT ERGNVRLSVIPTPTCDSPQMTAPSLDDDG  
WATVGVVIIAVVCVVGTSLVWVVIIYHTRRRNEDCSITNTDETNPADIPSYLSSQGLTAD  
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSS EADVEAATDLFLCPLGSGTGP  
MYLKGNVYGSDPFETYHTGCS PDPRTVLMDHYEPSYIKKKECYCPSHPSEESCERSFSNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD F SANPEPASVASSNSFMGTFGKALRRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQS  
YDLDT

### Signal sequence:

amino acids 1-19

### Transmembrane domain:

amino acids 746-765

### N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### Glycosaminoglycan attachment site.

amino acids 826-830

### Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### Tyrosine kinase phosphorylation site.

amino acids 607-615

### N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

# FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAATG  
AAGGATGTCAGGACCGCAGCTTCTCCCTGGAAACCGAACCGCAATGGATAAACTGATTGTGCAAGAGAGGAAGGAAGAAC  
GAAGCTTTTTCTGTGAGCCCTGGATCTTAAACACAAATGTGTATATGTGACACACAGGGAGCATTCAAGAATGAAA  
TAAACCCAGAGTTAGACCCCGCGGGGTTGGTGGTCTTGACATAAAATAAATACTTAAAGCAGCTGTTCCCTCC  
CCACCCCAAAAAAAGAGATGATTGGAATGAAGAACCAGGATTCACAAAGAAAAAGATGTTCATTTTTCTC  
TATAAAGGAGAAAGTGAGCCAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTATGTAAGTAAAGAAAT  
GGTGGTGGTGGTGGTCTTCTTCTTTTGAATTTCCCAACAGAGGAGAGGAAATTAATAATACATCTGCAAGAAAA  
TTTCAGAGAGAAAAATTGACCGCGGAGATGGAGCATTGATGGGGGAGAGAAACAGCAGAGCACAGTTGGA  
TTTGTGCTATGTTGACTAAAAATTGACGGATTAATTGCAGTTGGATTTTCTTCATCAACCTCCTTTTTTAAAT  
TTTATTCCTTTTGGTATCAAGATCATGGCTTTCTCTTGTCTTAAACCCTGGATTTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACGTGTTGAATCCAGAAGGACCAACACAGATAAATATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGGCCCTATTGACCCCTGCTTGTGGTCT  
GCTGGCTCTCAACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGTGCTCTGCAGCAA  
CCAGTTTCAGCAAGGTGATTGTGTTTCGGAACCACTGCGTGGGTCCGGATGGCATCTCCACCAACACAGCGCT  
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCATCTGGAATCCT  
ACAGTTGATAGGAACCATATCAGAACCATGAAATGGGGCTTCAATGGTCTGGCGAACCTCAACACTCGGA  
ACTCTTTGACAACTCGTCTTACTACCATCCCGAATGGAGCTTTGTATACTTGTCTAAATGGAAGGAGCTCTGGT  
GCGAAACACCCCAATTGAAGCATCCCTTCTTATGCTTTAAACAGAATTCCTCTTGGCCGAGCTAGACTTAGG  
GGAATTGAAAGACTTTCATACATCTCAGAAGGTGCCTTTGAAGTCTGTCCAACTTGAGGTATTGAACTTGC  
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTCTGGGAATCA  
TTTATCTGCCATCAGGCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAACTGTTGGATGATACAGTCCAGAT  
TCAAGTCTGATGAACGGAATGCCTTTGACAACTTCAGTCACTAGTGGAGATCAACCTGGCACACAAATATCTAAC  
ATTACTGCTCATGACCTCTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCACAACTTGGAACTG  
TAACTGTGACATCTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCGGTG  
TAACTCTCTCCCAATCAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCATGCTATGCTCCGTG  
GATTGTGGAGCCCCCTGACAGCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCCTCACATC  
CCTGACATCTGTATCTTGATTATCCCAAATGGAAACAGTCATGACATGGGGCGTACAAGGTGGCGATAGCTGT  
GCTCAGTGTGTGTACGTTAAATTTCACAAAATGTAACGTGTGCAAGATACAGGCATGTACATGATGTTGAGTAA  
TTCCGTGGGAATACTACTGCTTCAGCCACCCTGAATGTACTGCAGCAACCACTACTCCTTTCTTACTTTTC  
AACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGCGACGACCAAGATAACAATGTGGGTCCCCTCC  
AGTGGTCGACTGGGAGACCAACATGTGACCACTCTCTCACACACAGAGCACAAGGTGCAGACAGAGAAACCTT  
CACCATCCAGTGACTGATATAACAGTGGGATCCAGGAATGTGATGAGTCAATGAAGACTACCAAAATCATCAT  
TGGGTGTTTTGTGCGCTCACATCTGCTGAGTGTGCTGGTCAATTTACAAAGTGAAGGAGAGCAGCAACCA  
TCGGGAAACCATCTGCGCCCAACAGGACTGTTGAAATTTAATGTGGATGATGAGATTCAGGAGACACACCC  
CATGCAACCACTGCGCCATGCTGCTATCGAGCATGAGCACTAACTACATATACAAATCTCCCTT  
CAACCAACACAAACAGTTAAACAAATAAATTAATAACAGCTTCAAGTGTGATGAAACCGTTATGATCCGAATGAA  
CTCTAAAGCAATGTACAAGAGACTCAAACTTAAACATTTACAGAGTTTACAAAAACCAACAAATCAAAAAAAA  
GACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTACAAAAAACAA  
AAAGAGAAAGAAATTTATTTATTAATAATCTATTGTGATCTAAAGCAGACAAAA

## FIGURE 104

MLNKMTLHPQQIMIGPRFNRLFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGIISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNPNIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL  
LKSATSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNTVQDTGMYTCMVSNSVGN  
TTASATLNVTAATTPFSYFSTVTVTETMEPSQDEARTDNNVGPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDEITGDTMPESHLPMPAIEHEHLNHYNSYKSPFNHTTTVTNTINSIHSS  
VHEPLLRMSKDNVQETQI

### Signal sequence:

amino acids 1-44

### Transmembrane domain:

amino acids 523-543

### N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

### Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537



# FIGURE 105

AGCCGACGCTGCTCAAGCTGCGCAACTCTGTTCGAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGCGCA  
TGAAAGGGGTTCCGCCGCGGGAGTAAAAGAAAGGAATTGACGGGCGAGCGCGAGGGAGGAGCGCGCACGCGGACGCG  
GAGGGCGCGCTGGCAACCTTCGGCTGGAAGTTTGTGCGGGGCCCCGAGCGCGCGCGCTGGGAGCTTCGGGTAGA  
GACCTAGGCGCTGGGACCGCGATGAGCGCGCGAGCCTCGTGCGCCGCGCGCGGGTGGGGCTGCTGCTGTGTC  
GCGTGTCTGGGGCGCGCTGGCGGGTCCGACAGCGCGCGTTCGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCGCGC  
GAGCGCCCATCCGCCATACCTTGCCTGCTCGGGGACCTTGCTGGACTCGAAGCTGTAAGCGGGTTCGCGGCTCTT  
CAGCGGCCATCTCCGCTCTGGTGCCTGGCTGGACTTAAGTCAACAAGATTATTTTATCAAGGCAAGTTCC  
ATGAGGACCACTTCAAGGCTTCGAGAAGTGAACCGAAGTGAACCAAGTGAATTCGAAGTTCGAAGTTCGAGGACCT  
GCTCTGGCAATATTACACTTCTCTCTTGGCTGGAACAGGATTGTGAAATCTCCCTGAACACTTGAAGAG  
TTTCAGTCCCTTGAATCTTTGGACCTTAGCAGCAACAATATTTAGAGCTCGAAGCTTCGATTTCCAGCCTTCAG  
CTCAAAATATCTGATCTCTACAGCAACCGAGTCAATCAATGGAACCTGGGTATTTTGAACATTTGGGCAACACA  
CTCTCTGTGTAAAGCTGAACGAGAACCGAATCTCAGCTATCCACCAAGATGTTTAAACTGCCCRAAGCTGCA  
CATCTCGAATTGAACCGAAACAGATTTAAATGTAGATGGAAGTCAAGGCTTGGTGTCTGAGTCTGGAAGTCT  
CTGAAAATGCAAGAAATGGAGTAAAGAACTTATGGATGGAGCTTTTGGGGCTGAGCAACCTGAGGCGCATGTATCTC  
CAGCTGGACCAATAACCACTTACAGGATTACCAAGGCTGGCTTTTGGGGCTGAGCAACATGGAATTTTGG  
CTCAGCGCAAAATGCCATCAAGCAGGATCAGCCCTGATGCTGGGAGTTCTGCCAGAAGCTCAGTGAAGCTGGACCTA  
ACTTTCAATCACTTATCAAGTTGATGATTCAAGCTTCTTGGCTTAAGCTTATCAATACTGCATCTTGGG  
AACACAGAGTCAGCTACATTTGCTGATTGTGCTTCCGGGGCTTCCAGTTTCAAGACTTTGGATCTGAAGAAC  
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGTCTTCTCGGGCTGACAACTGAGGCGCATGTATCTC  
CAAGGAAATCGGATCCGCTCTATTACTAAAAAGGCTTCACTGGTTTGGATGATTTGAGACTCTAGACGATCT  
GACACGCAATCATGCTCTTTACAGGCAATGCATTTTCAAAATGAAGAACTCGACCAATTCGATTTTAAATACA  
TCAAGCTTTTGTGCGATTGCCAGCTAAATGGCTCCCAAGTGGGTGGCGGAAACCACTTTACAGACTTTGTA  
AATGCCAGTTGTGCCATCTCCAGCTTCAAAAGGAAGAAGCATTTTTGTCTGTAGCGCCAGATGGCTTTTGTGT  
GATGATTTTCCAAACCCAGATCAAGGTTGAGCGGACACAGTGGGCAATAAAGGTTTCAATTTGAGTTTCT  
TATGTCTCAGCTGCCAGCAGATGTATTTCCCAATGACTTTTGTCTGGAAAAAGACATTTCAACTCTCGCAT  
GCTGAAATGGAATAATATGCACACTTCCGGGCCCAAGGTGGGAGGTGATGGAGTATACCACTCTCCGCTGAT  
CGCGAGGTGGAATTTGCCAGTGGGGGAAATATCAGTGTGTCATCCCAATCACTTTGGTTTCACTCTACTCTGT  
AAAGCCAAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGAATCTACCATCCGAGCTGGGGC  
ATGGCAGCTGTGAGTGTGCTGCTGTGGGGCAACCCAGCCCGAGTAGCTGGCAGGAAGGATGGGGGCAAGAC  
TTCAGCTGCGCGGAGAGACGATGATGTGATGCGCCGAGGATGACGTGTTTCTTATCGTGGATGTGAAGATA  
GAGGACATTTGGGTATACAGCTGCACAGCTCAGAAGAGTATTCAGCAATGCAACTCTGACTGTCT  
CTAGAACAACCATCATTTTCTGGGCCACTGTTGGACCGAAGCTGTAACCAAGGGAGAAACAGCCGCTCTCAGTGC  
ATTTCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGAACCAAGATGATAGCCCATTTGGTGTAAACCGAGAGGCAC  
TTTTTTGCGAGCAGGCAATCAGCTTCTGATATTGTGACTCAGATGTGAGTGTGCGGAAATACACATGTGAG  
ATTTCTAAACCTCTTGGCACTGAGAGGAGAAACGTGGGCTCAGTGTGATCCCCACTGCAACCTGCGACTCCCT  
CAGATGACAGCCCATCGTTAGACGATGACGGATGGGGCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTCTGT  
GTGTTGGGCAAGCTCACTCGTGGGTGGTTCATCATATACCAACAGCGGAGGAATGAAGATTTGAGATTAAC  
AAGCAGATGAGACCACTTGGCAGCAGATATTCCTAGTTATTTGTGATCTCAGGGAACGTTAGCTGACAGGAG  
GATGGGTGAGTGTCTTCAAGAAAGTGAAGCCACCAACAGTGTGTCACATCTCAGGTCTGGATTTTCTTACCA  
CAACTACAGATGAGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGAAGCTGCCACAGATCTGTTCT  
CTTTGTCCGTTTGGGACTCAGAGCCCTATGTATTTGAAGGAAATGTGATAGCTCAGATCTTTTGAAGAA  
TATCATCAGAGTTGACGCTTGCACCCCAAGACAGTTTAAATGGACCACTATGAGCCAGTTACATAAGAAAAAG  
GAGTGTATACCAATGTTCTATCTCTCAGAAGAACTCTGCGAACGAGCTCATGATATATCTCGTGGCTTTACAT  
GTGGAAGAGTCTATTAACACTAGTTACTCTCAAAATGAAGACCTGGAATGAAAAATCTGTGCTCAAAACAGTCC  
CTTTTGAATTTAGTGGCAATCTGAGAGCCAGCGTGGTGTCTCGAGTAATTTCTCATGGGTATCTTTGGAAGA  
GCTCTCAGGAGACCTTCACTAGTGCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCAGGAGGCTTTTAT  
TGAAGACTCATTTCTTCCCAAGCTTGGACTCTGGGTGAGGAAAGATGGAAGGACAGATTTTCAAGAA  
GAAATACATTTTGTACCTTTAAACAGACTTGAAGAACTACAGGATCTCAAAATTTTCAAGCTTATGATCTGGAC  
ACATAGACTGAATGAGGACCAAGAAAGGCTTAACTACTACTCAAGTGAAGCTTTTATTTAAAGAGAGAGAAAT  
CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAATGCTTTATTTATACAGATGAACCAAAATTTG  
AAAAAGTTATGAAATTTTTATACCTGGGAATGATGCTCATATAAGAAATACCTTTTAAACTATTTTAACTTTG  
TTTTATGCAAAAAGTATCTTACCTAAATTAATGATATAAACTAGTATTTTATGTATTTTATAATGGCAGA  
TTCTTTTATGAAAAATGAGTTACTAAAGCATTTTAAATAATCTGCCTTTGTACCATTTTATAATGAGAGTT  
ACTCTATTATTTTGCACATTATATTTAATAAATGTGCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR  
KRLARLPEPLPSWVARLDLSLHNRSLFIKASSMSHLQSLREVKLNNLEETIPNLGPVSA  
LLSLAGNRIVEILPEHLKEFQSLLETDLSSNNISELQTAFAPALQKLYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNISAIIPKMFKLPLQLHLELNRRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWAFEC  
QKLSLSDLTFFNHLRLDDSSFLGLSLNLTLIHGNRRVSYIADCAFRGLSSSLKTLDLKNNFIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRSIYKKAFTGLDALEHLDDSDNAIMSLQGNAFSQMK  
KLQQLHLNTSSLLCDCQLKWLQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD  
PKPQITVQPTQSAIKGSNLSEICSAASSSDSPMTFAWKDKNELLHDAEMENYALHRAQGG  
VMEYTTILRLREVEFASGEGKYQCVISNHFSGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDDGTFPAARERRRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPKLNWTKDDSPLVVTERHF  
FAAGNQLLIIVSDSDVADAGKYTCMSNTLGTGERGNVRLSVIPTCDSPQMTAPSLDDDGWA  
TVGVVIIAVVCCVVGTSVLWVVVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTADRO  
DGYVSSSESGHHQVFTSSGAGFLPQHDSSGTCCHIDNSSADVEAATDLFLCPLFGSTGPMY  
LKGNVYGSDFETIYHTGCSPPDRTVLMDHYEPSYIKKKECPCSHPSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPKMKNCLNKKSSLDIFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLDGSGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQSYDLDT

### Signal sequence:

amino acids 1-27

### Transmembrane domain:

amino acids 808-828

### N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

### Glycosaminoglycan attachment site.

amino acids 886-890

### Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

### Tyrosine kinase phosphorylation site.

amino acids 667-675

### N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

### Leucine zipper pattern.

amino acids 58-80, 65-87

# FIGURE 107

CAAAACCTTGGCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCGAGGCCGCGGAGCGCAGCTGAGAC  
 TGGGGGAGCGCGCTTGGGCTCTGTGGGCGCCGCTCGGCGCGGGGCGCAGCAGGGAAGCTGTGGTCTGCC  
 CTGCTCCAGCGAGCGCCACTGGTGTGAACCGGAGAGAGCCCTGGTGGTCCCGTCCCTATCCCTCCTTTATATA  
 GAAACCTTCCACACTGGGAAGGCGAGCGCGCAGGAGGCTCATGGTGAAGAGGAGCGCGCTGCTGAG  
 GCGCACAGCATTCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCCTGCTGGT  
 TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGSCAACATGGCCAGAGCCGCGGTGGTGC  
 TGCCTCTGCTGTGCTGGCGCCAGCTGCACCTGGGACCTGTGCTTGGCTGAGGGGCCAGGATTTGGCGGAA  
 GTGGCGGCCACAGCTGAGCCCGAAGAGAACGAATTTGGGAGGAGGAGCGGTGCTGGTACTGAGCCCTGAGG  
 AGCCCGGGCTTGGCCAGCGCGGTGAGCTGGCCCTGGAGACTGTGCTGTTCAGGAGGGCGTGTGGAGCTGTG  
 GCGGTATTGACTCGCTGAGTTTCCCGGGGAGCCTGCTGAGCACACCAACCACTATCTCTGCAGAACCAACGAG  
 TGGAAAAGCTACCTGAGGAGCTCTCCGCGCTGCACCGGCTGGAGACTGAACTTGCAAAAACCAACCGCTGA  
 CTTCCCGAGGGCTCCAGAGAAAGCGTTTGAAGCATCTGACCAACCTCAATTAACCTGTACTTGCCCAATAAACA  
 TGACCTTGGCACCCCGCTTCTTGGCAACGCCCTGATCAGTGTGGACTTGTGCTGCAACTATCTCACAAGATCT  
 ATGGGCTCACCTTGGCCAGAAAGCAAACTTGAAGTCTGTGTACCTGCACAAACAAGCTGGCAGACGCGGBC  
 TGCCGAGCAACATGTTCAACGGCTCCAGCAAGCTCGAGGTCTCTGCTGCAGCAACTCTCTGCGCCACGCTGC  
 CCAAGCAGCTGCGGCTGCCCTGTACAAGCTGCACCTCAAGAACCAAGCTGGAGAAAGTCCCCCGGGGGCTGC  
 TCAGCGAGCTGAGCAGCTCGCGGAGCTATACCTGCAGAACCACTACCTGACTGACGAGGGCTGGACAACGAGA  
 CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCAGCTGGGCTGC  
 CGCGAGCTGGTGTGCTGCACTTGGAGAAGAACCCATCCGAGCGTGGACGCGAATGTGCTGACCCCCATCC  
 GCAGCTGAGTACCTGCTGTGTCACAGCAACAGCTCGCGGAGCAGGGCATCCACCACTGGCCTTCCAGGGCC  
 TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCTGGCCAGTGGCTGCCCTGCGCGGCTGC  
 GCACCTCATGATCCTGCACAACAGATCAAGGCAATTGGCGCGAAGACTTGGCACCACTACTCTCTGGAGG  
 AGCTCAACTCAGTCAACAGCTCACAGGCCACAGGTGCACGCGAGCGCTTCCGCAAGCTGCGCTGTGCTGC  
 GCTGCTGAGCTGTGGGCAACCGGCTGCACACGCTGCCACTTGGGCTGCTCGAAATGTCCATGTGCTGAAGG  
 TCAAGCGTATGAGTGGTGCTTGGCAGGAGGGCGCTGGCGGCTGCTGAGTACCTGTACTGCAGAACCAACA  
 CCAAGCAACGCTGCGCAGCGAGCCCTGGGCGCCCGTGGCTGGGTGAGCTTGCGCCATCTGCAGCTGCTGGACA  
 TCAGCGGAAATCAGCTCAGAGAGTCCCGAGGGGCTCCCGAGTCACTTGAGTACCTGTACTGCAGAACCAACA  
 AGATTAGTGGTGGTGGCGGCAATGCTTGAAGCTCAACGCGCAACCTCAAGGGGATCTTCTCAGGTTTAAACAAG  
 TGCTGTGGGCTCGTGGTGCAGTGCCTTCCGAGGCTGAAGCACTGAGGATCTTGGACATTGAAGGCACT  
 TAGAGTTTGGTGAATTTCCAGGACCGTGGCGCTTGGGGAAGGAAAGGAGGAGGAGGAGGAGGAGGAGG  
 AGGAAGAGGAAACAAGATAGTGAAGGTGATGAGATGTGAAGTGGATGGAACCGCGGAGCTCTTTCTGTCG  
 AGCACAGCCTCTGTGCTGTGAGCCCCCACTCTGCGTGTCTACACAGACACACCCAGCTGCACACATGAGGCA  
 TCCCATGATGACACGCGCTGACACAGTCTCATATCCCCACCCTTCCACGGGCTGTCCACGCGCAGACATGAC  
 ACACATCAGACCTCCAAACCCAGCTCAGCCACACAACTACCTTCAAACACCAACAGTCTCTGTACAC  
 CCCCACATACCGCTCAAACGCCCTCTGAATCATGACGGGAAGGCTGCGCCCTGGCTGGCAACACAGGACCCCA  
 TCCCCCTCCCCCTGTGACTGTGTATGCGTATGCATACACACCAACACACACATGCACAAAGTATGTGCGAA  
 CAGCCCTCCAAAGCTCATGCCACAGACGCTCTTGGCCAGCAGAGCTAGCAGCTGCGCCCTGCGCCCT  
 GTCCATCTGTGCGTCCGTCCCTGGAGAGACCAAGGATATCATGCTGTGGGACAGGAGTCTGCGCACCTCT  
 GGAATCACAAGAGCTGCTTCCCTTATCTTCTTCCATCTATGGGGAAGGAGCTTCCAGGATGCTGGGCTGGCC  
 TGGCCACCTCTGCTCCAGGTGCTGGGAGTCACTCTGTAAGAGTCCCTCCCTGCCAGCCCTGGCAGGACA  
 CAGGACTTTTCCAATGGGCAAGCCAGTGGAGCAGGATGGAGAGGCCCTGGGTGCTGTGCGGGCTTGGGG  
 CAGGATGAAGCAGAGGTGATGGGCTGGCTGAGCGAGGAGGAGGAGCCCTGGGTGCTGTGCGGGCTTGGGG  
 GTTCTTCAGGCTGTGGGGAAGTTCGGGGTGCCTTTATTTTATCTTTTCAAGGAAAAAATGATAAAAAAT  
 CTCAAAGCTGATTTTCTGTTATAGAAAACTAATAAAGCAATATCCCTATCCCTGCAAAAAATAA

## FIGURE 108

MEGEEAEQPAWFHQPWRFPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPREENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDGCGIDLREFPGDLF  
EHTNHLSLQNNQLEKIYPEELSRHLRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFMNGSSNV  
EVLILSSNFLRHVPKHLPPALYKHLKNNKLEKIPPGAFSELSSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSPQVHRDAFRKLRLRLSRLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

GGAGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCTCGGAGAGGGGCAC  
CGATAGGCCCGGGCGGGAGGCTGTGGGGTGTCTCGAGACTCTCAGAGGGGCGCTCCATCGCGCCACCAACGCT  
CAACCTGTCTTCGCGCGAGCTGCGCTGCGCCGACAGGCCGTGCCCAACATGAATGATTTTCTCTGGCCCTGCT  
CTGTGATATCTCGCTCATCTGCTGAGCGCGCGCCGAGTTCAGCGAGGAGGTGGCCAGGAAAATAGTGTTCATCGAT  
TGCCCTATGTCTGTATTGTTGGGAGGATTTGACTGTCTGGGGCTGGGCTGCCAGCTCTGGGGACAGTGTGCACGC  
TGTGTGCCAACACAGTGCACCAACATAGTGAATGTATCGCGCCAAACAGTGCAGGTGATCTCTGGTTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATAGTGTGGCTCGAAGCCCGCCCTCTAAGCACAGGTGCATGAACACTT  
CGCGACCTCAAGTGTCTACTGTCTCAACGAGTATATGCTCATGCGCGATGTTCTCTGCTCATAGTGCCTGACCT  
CTCCATGCCAACACTGTTCAGTATGCTGTGATGTTTAAAGGACAAATACGGTGCAAGTGGCCATCCCTTGGCC  
GCACCTGGCTCTGTATGGGAGGACCTGTGATATGTTGATGAATGTGTCAAGGAAGAGCTCTCTGCTGATTTAGT  
TAGGCAATCTGTCAACATTTTGGGAGCTCATGTGCAAGTGTCAAAAGCTTGATCTCATGTATATTGGAGG  
CAAAATCATCAATGTACATGATAGCAAGTCTCACTTGGTCAGTTCAGTGCACAGCTTTGCTCGATGTTATTAAC  
CTACGTGGGTCTCAACAGTGCAAATGTAAAGAAAGGATACAGGTTGTAGACTCATTTGTGTATATCCAAA  
ATATTATGATGAACCTTCAGGTGCAAAATCTGTACCAAAGGGAAGATGGTACCATTTTAAAGGGTGACACAGGAA  
TAATAATTGGATTCCTGATGTTGGAAGTACTTGGTGGCTCCGAAGACACATATATCTCTCTATATACCAA  
CAGGCTACTCTTCAAGCCAAACAAAGACTCACCAACCGCAACCAAAATCTCTACTCCACCAACCAACCAAC  
CTCTCCCAACAGAGCTCAGAACACCTTACACCTACCAACCCGAAGGCGCAACACCGGACTGACAACTATAGC  
ACCAGCTGCCAGTACACCTCAGGAGGGATACAGTTGACAAACAGGTCACAGACAGCTCGAACCACCCAGAG  
AGATGTGTTTCAGTGTCTGTGATCAAGCTGTAATTTGACATGACTTTGTGATGGATTGAGGAGGAAGAACAA  
GACTGTGACTGGGAACCACTCAGGAGCCAGCGAGTGGACAAATCTGACAGTGTGGGCGCAACCGCCCGAG  
GGGAAGAGCTGCAGCTCTGGTCTACTCTCCGCGCTCATGCTTACAGGAGTCTGGCTGTCTATCAGGCA  
CAGGTGTGACGGGGCTGCACTGTGGCTCAGGTGTTGTGAGAAACACCGTGGCCACGCGAGCGCTCTGTG  
GGGAAGAGAGTGGTGCCCTGGCTGAGGCAAAACAGATCACTTGCAGGGGGTGACATCAAGGCAATCAACA  
AAGATGAATTAAGGGTTTGA AAAA AAGATCATATGATGAAATTAAGGAATCGGGATCTCTTCTCTGGAGAG  
AGAAAGCTGAGGGGCAAAACATTGTAGTTTTCAGTATATAAGAGTTGGCCACAGAGAGGTGGCCACAGCTG  
TCTCCATATGCACTAAGATATAGAACAGGAGGAACTGGCTTAGACTAGATATAAGGAGATCTTTCTGGCAG  
GGCCATTTGTAGATATCTCATATAAAAGGAAGTGTGAAATCTCAGTATATCTCTCTCTTAAAAAATTAGA  
TAAAAATTTGTCTATTTAAGATGTTTAAAGATGTTCTTCCACCAAGGAAAAGTAACAAATTATAGAATTTCCAA  
AGATGTTTGTGATCTCATAGTATGATGCAGTGAATTTCTTAGAAGCTAAATTAATTTGAACCTTAATTTAGG  
CATTTCCCTCTTGACCTCTATAAGGAGGGATTTGAAGGGGAAGGCGCCAACTCAGCTCTGACCTCATGTAAT  
TCTTCTCCCTTTAGGCAATCTAGCAATATTAAGAAAGAAAGAAATCTATTATTTCAATGACAGTATGATGAGC  
AGATATTTTAGATTTCTCATGATATGCTAGTGTGGGGTGGTTTTCAGTGTTCCTCATGGTAAAGGATATAGGCC  
TTCATTGTTCTCAATGATGATGTTTCAGATTTTCTTTTAAAGAGATCTTCAAGGAACAGCTGCACAGAG  
ATTTTCTACGGGTGATCTTCTCTGCTCTGTGTGACAGTATATCTTGCTGTGAGAAAGGTGCGCTGCCCC  
ACACCGGCAAGATTTCTCTTCACTCATCAGTATGATCAGTTTCTCTTATCAATTGGACTCTCCGAGCTCCAC  
AGAACGTAACTATTTTGAACAAATAGTGAACAATGAAGGTTCTTCTGCTCATTTAACTGTGTAAGGAGCGGCTCG  
AGGGGGAAAAATAATCATTAAGCCTTTGATGTAACGCGAGAATATAGGCTGTAGATCCATTTTAAATGGTCTGT  
TCTTTATGTTGATACATATACGTGCACAGCTGAAGATGAAGGGGAAAAATAAGGAAATTTACTTTTTCATGGCAA  
TGATACATTCAGCTAATACTGATGGGAAGATTTACAAAGTACGTATATACATCTGTTTATTTTAATGTTT  
CTAAATAAAAAATTTAGTGGTTTCTTCAAATGGCCATAATAAAAAAACTATTTGTAATAAAAAACCTTTAGTAA

## FIGURE 110

MDFLALVLVSSLYLQAAAAEFDRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDDVVKQIRQCPSPLGLHAPDGRTCVDVDECATGRASCPFRQC  
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNWIIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPTPTTGLTTIAPAASTPPGGITVDN  
RVQTDPPQKPRGDVFSVLVHSCNFDHGLCGWIREKNDLHWEPIRDPAGGQYLTVSAAKAPGG  
KAARLVLPLGLMLHSGDLCLSFHVKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHWRTQI  
TLRGADIKSESQR

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 273-277

### **Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

### **Tyrosine kinase phosphorylation site.**

amino acids 199-206

### **N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

### **Cell attachment sequence.**

amino acids 382-385

### **EGF-like domain cysteine pattern signature.**

amino acids 75-87

# FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGCCCCCTTAGATTGTGA  
**AAATG**TGGCTCAAGGCTTTCACAACCTTTCTCTTTGCAACAGGTGCTTGCTCGGGGCTGA  
 AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCCTCTACCTACCCGTC  
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
 CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTGTGACTTGGGAATACC  
 AACACAAGTTCCACATGATGCCACCCAAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTCT  
 GATGAAGGCAATTACATCGTGAAGGTCAACATTACAGGAAATGGAACCTATCTGCCAGTCA  
 GAAGATACAAGTACGGTTGATGATCCTGTCAAAAGCCAGTGGTGAGATTATCCTCCCT  
 CTGGGGCTGTGGAGTATGTGGGGAACATGACCTGACATGCCATGTGGGAAGGGGGCACTCGG  
 CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
 TCCCCAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
 GCCTGGTGAGGAACCTGTGAGTAAATGGAAAGTGATATCATTATGCCCATCATATATTAT  
 GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTCTTACTGT  
 TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGTGATTCTCATCCCCCAACACCTACT  
 CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCTCGTTAGAAGTT  
 GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTCTGTGCTTACAACAACATAAC  
 CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
 CACAGAAAGGAAAATCATTGTCACTTTAGCAAGTATAACTGGAATATCATAATTTTGATT  
 ATATCCATGTGCTTCTCTTCCATATGAAAAAATCAACCTACAAAGTTATAAAACAGAA  
 ACTAGAAGGCAGGCAGAAACAGAATACAGGAAGGCTCAAACATTTTCAGGCCATGAAGATG  
 CTCTGGATGACTTCGGAATATATGAATTTGTGCTTTTCAGATGTTTCTGGTGTTTCCAGG  
 ATTCCAAGCAGGCTGTGTTCCAGCCTCTGATTGTGTATCGGGCAAGATTGTCACAGTACAGT  
 GTATGAAGTTATTAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTTTCATGG  
 GCTAAACAGTACATTGAGTGAAATCTGAAGAAACATTTAAGGAAAAACAGTGGAAAAGT  
 ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTTATCCTTTACA  
 TGCAGAAATAGAGGCATTTATGCAAATTGAACCTGCAGGTTTTTCAGCATATACAAATGTCTT  
 GTGCAACAGAAAAACATGTTGGGGAAATATCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
 GGAGAACGAAAGTGACAGGGGTTTCTCATAAAGTTTGTATGAAATATCTCTACAAACCTCA  
 ATTAGTCTTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
 TGTGGAACCTTTACATTGTTTCGATTTTTCAGCAGACTTGTGTTTATTAATTTTATTAGTG  
 TTAAGAAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTATTGTACAA  
 CAAAGTAATAAGGATGGTTGTACAAAAACAAAACATATGCCTTCTCTTTTTTTTCAATCACC  
 AGTAGTATTTTGTAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTAA  
 TTTTTTCAAGGAAAGATGGATTCAATAAATTATCTGTTTTGCTTTTAAAAAATAAAAAA

## FIGURE 112

MWLKVF<sup>1</sup>TTFLSFATGACSGLKVTVP<sup>2</sup>SHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSV<sup>3</sup>VPDLEYQHKFTMMFPNASLLINPLQFPDEGNYIVKVNIQGN<sup>4</sup>GTLSASQ  
KIQVTVD<sup>5</sup>DPVTKPVVQIHP<sup>6</sup>PSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSE<sup>7</sup>MESDIIMPIIYGYGPLYGLQVNSDKGLKVGEVFTV  
DLGEAILFD<sup>8</sup>CSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTV<sup>9</sup>IITSVGLEKLAQKGKSLSP<sup>10</sup>LASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSR<sup>11</sup>SVPASDCVSGQDLHSTV  
YEVIQHIPAAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



# FIGURE 113

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGCACTTCCCCTGGCAGTCTCTGGTGTGTT  
GCTTTGGGGTCTCCCTGGACGCACGGGCGGGGAGCAACGTTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCTCTGCT  
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTCGCTGAATGGGGAGAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC  
TTCCTACTATTTATCATTTGTAAGATGGTGAATTTAGGCGCTATCAGGCTCCAAGGACTAAG  
AAGGACTTCATAAATTTTATAAGTGATAAAGAGTGGAAAGATTTAGAGCCCGTTTCATCATG  
GTTTGGTCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTTGTCTTAGCAACTCTGTTTTCCGGGACTGTTATTAGGACTCTGTATGATATTTGTGGC  
AGATTGCCCTTTGTCCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAT  
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAACAAGACTTCCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAAAGAGATTGATCATTGTTGTTGGTTTGAAGTG  
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTTGAAGAGTCTA  
CATTTCAGAACATAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTTTGAATAATCGTGCCAAAGCAATAAGATTATGATATTTGT  
TTAATAATAACCTATTTCAAGTCTGAGTTTGAATAATTTACATTTCCCAAGTATTGCATTAT  
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTCTCATTGATATAATTTTCTCTG  
TTTCACTGTGTGAAAAAAGAAAGATATTTCCCATAAATGGGAAGTTTGGCCATTGCTCAAG  
AAATGTGTATTTTCAGTGACAATTTCTGGTCTTTTAGAGGTATATCCAAAATTTCTTGT  
ATTTTTAGGTTATGCAACTAATAAAACTACCTTACATTAATTAATACAGTTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAAGTTTCATGGTATTCTCTGATTC  
CAACAAAGTTTGATTTTCTCTGTATTTTCTTACTTACTATGGGTACATTTTTTATTTTT  
CAAATTTGGATGATAATTTCTTGGAAACATTTTTATGTTTGTAGTAAACAGTATTTTTTGT  
GTTTCAAAGTGAAGTTTACTGAGAGATCCATCAAATGAACAATCTGTGTAATTTAAATTT  
TTGGCCACTTTTTTTCAGATTTTACATCATTCTTGCTGAACCTTCAACTGAAATTTGTTTTT  
TTTTTTTTTGGATGTGAAGGTGAACATTCTGATTTTGTCTGATGTGAAAAAGCCTTGGTA  
TTTTACATTTTGAATAATCAAAGAAGCTTAATATAAAGTTTGCATTCTACTCAGGAAAAAG  
CATCTTCTGTATATGCTTAAATGTATTTTGTCTCATATACAGAAAGTTCTTAATTGAT  
TTTACAGTCTGTAATGCTTGATTTTTTAAATAATAACATTTTTATATTTTTTAAAGACAA  
ACTTCATATTATCCTGTGTTCTTTTCTGACTGGTAATTTGTGTGGGATTTACAGGTA  
GTGAGTAGGATGGAACATTTTTAGTGATTTTACTCCTTAAAGAGCTAGAATACATAGTTTT  
CACCTTAAAAAGAGGGGAAAAATCATAAATACAATGAATCACTGACCATTACGTAGTAGAC  
AATTTCTGTAATGCTCCCTTCTTTCTAGGCTCTGTGCTGTGTGATCCATTGAATTTACAG  
TATCGTAATATCAAGTTTCTTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT  
AAAGAGTTTGGATGTGTAACCTGTGATGCCCTAGAAAAATATCCTAAGCACAAAAATAACCT  
TTCTAACCACTTCATTAAAGCTGAAAAAATTTTTTTTTT

## FIGURE 114

MAPSGSLAVPLAVLVLLWLGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFI~~SD~~KEWKSI~~EP~~VSSWFGPGSVLMSSMSALFQLSMWIR~~TCH~~NYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEEDVSE  
EEAESKEGTNKDFPQNAIRQ~~RS~~LGPSLATDKS

### Signal sequence:

amino acids 1-26

### Transmembrane domain:

amino acids 182-201

### Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

### Tyrosine kinase phosphorylation site.

amino acids 107-115

### N-myristoylation site.

amino acids 20-26, 192-198

### Amidation site.

amino acids 25-29

# FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTAACTAATTCAACAAACGGGACCCTT  
 CTGTGTGCGCAGAAACCGCAAGCAGTTGCTAACCAGTGGGACAGGCGGATTGGAAGAGCGGG  
 AAGGTCCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
 ATTGTCTGATGGCCTGGTGTGCTGAGCTGTGTGAGGCGGAATCTTACCTCTATTG  
 GGCACATGACTGACCTGATTATGACAGAGAAAGAGCTGGTGCAGTCTCTGAAAAGAGTACATC  
 CTTGTGGAGGAAGCCAAAGCTTCCAGATTAAAGAGCTGGGCCAACAAATGGAAGCCTTGAC  
 TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCTGTGAATGCCTACAACTGG  
 TGAAGCGGCTAAACACAGACTGGCTTGGCTGGAGGACCTTGTCTGAGGACTCAGCTGCA  
 GGTTTTATCGCCAACCTCTCTGTGAGCGGCAGTTCTTCCCACTGATGAGGACGAGATAGG  
 AGCTGCCAAAGCCTGTATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
 GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG  
 GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
 AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTACAGGTGCTGGACTACCTCA  
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCCTGGCCTGCTC  
 TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA  
 GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAGGCA  
 TCTATGAGAGGCTCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGG  
 GAGGGGTGCAAACTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA  
 CAGGGGCCACAGCTGCTTATTGCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA  
 TCGTCAGGTACTACGATGTCTGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
 CCTAACTTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCACTGTGCGCCAGCTA  
 CCGGGTTTCCAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC  
 GTCGGATGCAGCATATCAGAGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTGCAAAAT  
 TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG  
 CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACATACATGAGTGTGTAGAAGCTG  
 GTGGTGCCACCGCTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG  
 TTCTGGTACAAACCTCTTGGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCCC  
 TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACAGGAGGACGAGTTCT  
 TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCTTTTCTGTCCTTCCCTTCTGGTCT  
 CTTAGCCCATGTCAACGTGACAGACACTTGTATGTTCTTGTATGTTCTATCAGGCT  
 GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGAGACCATACTAGGCGACTCCTGT  
 GTGACTGAAGTCCCGACCTTCCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
 AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTTGTACCTCAGGTGTT  
 TTAGGTGTGAGATGTTTTCAGTGAACCAAGTTCTGATACCTTGTGTTACATGTTTGTGTTTAT  
 GGCATTCTATCTATTGTGGCTTTACCAAAAAATAAATGTCCCTACCAGAAAAA

## FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAALKMLRLQDITYRLDPGTISRGLPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDYLPEDVYESLCRGEVVKLTPTRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRMRQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSSLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTVEVD

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 115-119, 264-268

### **Glycosaminoglycan attachment site.**

amino acids 490-494

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

### **Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

### **Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

### **N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

### **Leucine zipper pattern.**

amino acids 213-235

# FIGURE 117

GCAGTATTGAGTTTTACTTCTCTCTCTTTTATGGAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT  
 TTCATTTATACCGTTTGTGGTGGGGTTAGTTCGACACCTTCACAGTTGAAGAGCAGGAGGAGTTGTGA  
 AGACAGGACAATCTCTTGGGGATGCTGGTCTCGAAGCCAGCGGGCTTGTCTGTCTTTGGCCTCATTGACCC  
 CAGGTCTCTGTGTTAAACCTGAAAGCCTACTACTGCGCTGGTGGCTCAATCCATTGATCTTGGGCTGTGCC  
 CCTGGGGCACCCACTTGGCAGGGCTTACCACCTGCGACTGAGCTCCCTGTGGCTCTGTGCGGCCAGCGCTTC  
 CCCTCATCTTAGGGCTGTCTCTGGGGTGAGCCTGAGCCTCTCGGGTTTCTTGGATCAGGGGGAGGGAAG  
 ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCAGATTCCAGAGCTCGGCTAGACCAAGT  
 ATGAAGACTTCAAACCCCGGATGTGCTCTACTACAGGAGCCCAACAGCCCTACAAGAAGGTGCTCAGGACTC  
 GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA  
 CTTTGGCCGTGGCTGTGAACCTACGCTGGGCCATCACTTCCCTCGGTACTCTACTCTGCGCAGCGGGGG  
 CCGGGCTCCAGCAGGATGACAGTGGTGTCTCATGGGATGAGCGGCCCGCTGGCTCATCTCAGAGACCCCTGC  
 GCCACCTTCAACACACTTTGGGGCCGACTACGATGGTTCTTATCATGACAGGATGACACATATGTGACGGCC  
 CCCGCTGGCAGCCTTGTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGAGAGGAGTTTCAATTG  
 GCGCAGGCGAGCAGGCCGGTACTGTCTATGGGGCTTTGGCTACCTGTGTGACGGAGTCTCTGCTTCTGTG  
 GGCCACATCTGGATGGCTCGCAGGAGACATTTCAAGTCCCGTCTGACGAGTGGCTTGGACCTGCTCATTTG  
 ACTCTCTGGCGCTCGGCTGTGTCTCAGACACCAGGGGAGCAGTATCGCTCATTTGAACCTGGCCAAATAGGG  
 ACCCTGTGAGAAGGAGGGAGCTCGGCTTTCTGAGTGCTTCCCGTGCACCTGTCTCCGAAGGTACCTCATGT  
 ACCGGCTCCACAACCGCTTACGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACACTCGAGGCTCAGA  
 TCCGAACCTGACCGTGTGACCCCGAAGGGGAGGAGGGCTGAGCTGGCCCTTGGGCTCCCTGCTCTTCA  
 CACCAACTCTGCTTTGAGGTGTGGGCTGGGACTACTTCAAGAGCAGCACCTTCTCTGTGAGATGGGG  
 CTCTCAAGTCCCCTACAGGGGGCTAGCAGGGGGAGCGTGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
 ATCGGCGCTACAGCCCGGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCAG  
 GGGGATGAGTACACCTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGGCAACCGGGGGCTGGCTCGCA  
 GGCTCAGCGTGTGCGGCCACTGAGCGGGGTGGAATCTTACTATGCGCTATGTCACTGAGGCCACCCGAGTGC  
 AGCTGGTGTGCTGCACTCTGTGGGCTGAAGCTGTGTCAGCCCGGGCTTTCCTGAGGCGTTTGGAGCAATGTC  
 TGGAGCCAGCAGAACATGCAATGTCTACCCCTGTGTGTGCTAGCGGCCAGCAGAGGTTGGCGTGGAGCTCCAG  
 ACCATTTCTTGGGCTGAAGCTGTCAGCAGCGGAGTTAGAGCGACGGTACCTGGGACGAGGCTGGCTGGCTCG  
 CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGAGCGTGGCTCGAAGAAGCACCCCTGTGGACACTCTCT  
 TCTTCTTACCAACCTGTGGAAGAAGCTGGGCCCCGAAGTCTCAACCGCTGTGCGATGAATCCATCTCTGGCT  
 ACCGGCAGGCTTCTTCCAGTCAATTTCCAGGAGTTCAATCTGCTGCTGACACAGAGATCAACCCCAAGGGCCCC  
 CGGGGGCTGGCCCTGACCCCCCTCCCTCTGCTGCTGACCCCTCCCGGGGGCTTCTAGGGGGAGATTG  
 ACCGGCAGGCTTCTGCGGAGGCTGTCTTCAACAGCTGACTACCTGGCGGGCCGAGCCGGCTGGCAGGTGAAC  
 TGGCAGGCGGGAAGAGGAGAACCCCTGGAGGGGCTGGAGGTGATGGATGTTTCTCCGGTTCTCAGGGCTCC  
 AACTCTTCCGGGCTAGAGCCAGGGCTGGTGCAGAAATTCTCCTGCGAGACTGACGCCACGGCTCAGTGAAG  
 AACTCTACCAACCGCTCGCCGCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCACGTGGCTATGGCTCTTTG  
 AGCAGGAGCAGGCCAATGACCTTAGCCCCCTGGGGCCCTAACCTCATTACCTTCTCTTGTCTGCTCAGCC  
 CCAGGAAGGGCAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTTAAATATGAAATGTTATTAA  
 ACATGTCTCTGCG

## FIGURE 118

MRLSSLLALLRPAALPLILGLSLGCSLSLLRVSWIQEGEGPCVEAVGERGGPQNPDSSRARLD  
QSDEDFKPRIVYYRDPNPKYKKVLRTRYIQTELGSRRERLLVAVLTSTRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRLHLTHFGADYDWWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQGGQYRSFELAKNRDPEKEGSSAFLSAFVAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGAPKCPLOQASRADVGDALTALEQLNRRYQPRLRFQKQRLNNGYR  
RFDPARMEYTLDDLLECVTQRGHRRALARRVSLRLPLSRVEILPMPYVTEATRVQLVLPPL  
VAEAAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGDPDPPSPGADPSRGAPIGGRFDRQSAEGCFYNADYLAA  
RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRALAMALFEQEQUANST  
Signal sequence:

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGGGCTGCGCTTTCCTGTCCCCAAGCC  
GTTCTAGACGCGGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTTCGAGTATACTGTATTATCCTTGTAAAACC  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACTGTGACAAAGCAG  
AGTTCCTTCAGTTCTGAAAATGTTAAAGTGTGTTGAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACGTG  
GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAAACCTAAAGTATTTTTTGTAA  
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGCTTAAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTTACTTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT  
GATGCATTGGTTTTCTTACCTCCAAATGGTTCGTACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA  
TACAGCTGTATGTTTCTTTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTTAAAG  
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTTAAACACATGAACATTGTAATG  
TGTTGGAAAGAAGTGTTTAAGAATAATAATTTGCAATAAACTATTAAATAAATATTATAT  
GTGATAAATCTAAATTATGAACATTAGAAATCTGTGGGACACATATTTTGTGATTGGTT  
AAAAAATTTTAAACAGGCTTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAACTTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
AAGCCTCCCCAAGTTCGAATGGATTGCCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAGTGAAAGTTGAAAAAT

## FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFVRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMRMRK  
AYKYAPDKYRDQYNWFFLARPTTFALIIENLKYFLKKDPSQPFYLGHTIKSGDLEYVGMIEGG  
IVLSVESMKRLNSLLNIPEKCPQQGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNNT  
KSVGLSIIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

### **Signal sequence:**

amino acids 1-33

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250



**FIGURE 121**

AAAAA

## FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNC SAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLED CATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

### Signal sequence:

amino acids 1-42

### N-glycosylation site.

amino acids 2-6, 62-66, 107-111

### Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

### N-myristoylation site.

amino acids 15-21, 74-80, 155-161

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCGCGCGCTGCCGCTGGCCCTCAGCAACCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTCGGCTCGGCTGCCCTGAGTCTTCTCTGCTGCTGCTTTTCAGGGGCTGCCGTATAGGGGCTGTAAATC  
TCAAAATCCAGCAATCGAAGCCAGCTGGTACAGGAATTTGAAAGTGTGGAACCTGTCTGTCACTATTACGGATTCCG  
AGACAAGTGAACCCAGGATCGAGTGGAAAGAAATTCAGAGTGAACAACCACTATGTGTTTGTGACAAACAAA  
TTCAGGGAGACTTGGCGGCTGCTGCAGAAATACCTGGGAAGACATCCCTGAAGATCTGGAAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGTCTGTCTGCTGAAATGACCGAAGGAATGTATGAGATTTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGAACCTGTCTGTAGAGTGCAGAGGCTGTACAGTAGGCAAGATGGCAACACTGC  
ACTGTCAGGAGAGTGGAGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGTATGATCTACCTGCCCACGGAT  
CCAGAGCAATTTCCGAGATTTCCGAATTTCTTCCACTTAAACTCTGAACAGGCACITTTGGTGTCTACTGCTG  
TTCACAAGGACGACTCTGGGCACTACTACTGCAATTCCTCAATGACCGAGGCTTCTGGTGTCTTGTCTGTGCTGCA  
AGATGGAAGTCTATGACCTGAACATTTGGCGAAATTTTGGGGGGTCTTGGTGTCTTGTCTGTGTACTGGCCCTGA  
TCACTGTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAAATAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGGACTTCAAGACAAAGTCACTGTTGA  
TGATCTGAGACCCCGGCTGTGCTGAGAGCGCACAGAGCGCAGCTGCACATACCTCTGTAGAAACTCTGTGTA  
GGCAGCGAGAGCTGTATGCACTCGGACGAGCTAGACACTCATTGAGAAGCTTTTCGTTTGGCCAAAGTTGACCA  
CTACTCTTCTACTCTAACAAGCCACATGAATAGAGAATTTTCCTCAAGATGGACCCGGTAAATATAACCAAA  
GGAGAGCAAACTGGGTGCGTCTCACTGAGTGTGGGTTCTTAATCTGTTTCTGGCCTGATTCGCCGATGACTATTAGG  
GTGATCTTAAAGAGTTTGTCTACGTAAACGCCCGCTGTGGGCCCTGTGAAGCCAGCATGTTCAACCACTGTGCTCT  
CAGCAGCCACGACAGTCCATGTAGATGGCGAGGTGGCTGGACAGCAAGCAGCAGGCTCCCGGCGGGAACCCA  
GAAAGGGTCTTTACACAGCAGCTTACTTTCATCGGCCACAGACACCCAGCAGTTTCTTCTTAAAGGCTCTGAG  
TGATCGGTTGTGAGTGTCCATTTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAACAAACCAAAATCAGGAAG  
GTAAATTTGTGCTGGAAGAGGGATCTGTCTGAGGAACCTGCTTGTCCAACAGGCTGTGAGGATTTAAGGAAA  
ACCTCTGCTGTTAGGCTAAGTCTGAATGGTACTGAATATGCTTTCTATGGGCTCTGTTTATTTTATAAAATTT  
TACATCTAAATTTTGTCTAAGGATGTATTTGTATTTATGAAAGAAAAATTTCTATTTAACTGTAAATATATTGT  
TACAATATGTTAAATAACCTATTTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT  
TGAAGAAATCAATAATTAAGAGTATTTTACCAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTCTTTCT  
CACAAGATTTTAGCCTTTTTCACAAGGGAACCTATACCTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTTCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAGAAACCTCTCAGTGTAGCTTTGAACT  
GCCTCTTCTGAGATGCTCAAGACGCTGTACCAGAGGCCACCCAGAAGGCTCAGATGTACATACACAGATG  
CCAGTCAGCTCTCGGGGTGGGCCAGGCCGCCCGCTCTAGCTCACTGTGTGCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGTGCTTACTCAGTGGGCCCTTGTCTCATCCAGCACAGC  
TCTCAGTGGGCACTGAGGAGCACTGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAAACAGACCTCT  
TTTGGTTATGATGGCTCACAAATAGGGCCCCCAATGCTATTTTTTTAAAGTTTGTTTAAATTAATTTGT  
AAGATTTGTCTAAGGCCAAAGGCAATGTGGAATCAAGTCTGTCAAGTACAATAACATTTTAAAGAAATATGGAT  
CCCAGTGTCTCTTTTGGCCAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAACAAACCAATGAT  
GGAGTGGCGGCCAGTCCAGCTTTTAAAGAACGTCAGGTGGAGCAGCAGGTGAAAGGCTTGGCGGGGAGGAAG  
TGAAACGCCCTGAATCAAAGCAGTTTCTAATTTTGACTTTAAATTTTTCATCGCCGAGAGACATGTGCTCCAT  
TGTGGGGGGAACATTAGCAACACTCACTCAGAAGCCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGCACTCAGGACTGAAGTGTGCTGAAGCAAGGAGCTGTGAGAAGGAGCCTCAGCTGTGTGCTGGA  
GAATGGCTCTCACTACTCACTCTGTCTTTCAGTCTCCAGTGTCTTGGGTTTTTATACTTTGACAGCTTTTTTT  
AAATGTCATCATGAGACTGTGTGACTTTTTTGTATGTGTGAACACTTTCGCCAGGCGGCCCTGGCAGAGGCA  
GAGAAATGCTCCAGAGTGGCTAGTGTCTCCCTGGTGTCTGTGTCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTTGCCACTCTTGTGAGAGGAGTGGCTGCCACCTCAGGCTCAGGTTACGCTTAACTAGGACTAGA  
CTCTTGTGTGTCATAGTGAATGGGAGCTTATTGGCCCCCTCTTCTTATACCTTAAACCTTCTACACTAGTGCCA  
TGGAACCAAGGCTCTGAAAGAGTGAAGAGAGTGAAGTGAAGTGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATCT  
CGGAAAGGAATACTCTGTGATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATCT  
GCCTTTGGATGATGTTGCTGTACAGACTGTACAGACTTGTACTAACACCCGTAATTTGGCATTGTGTTAAC  
CTCATTTTAAAGCTTCAAAAAACCA

## FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624  
><subunit 1 of 1, 310 aa, 1 stop  
><MW: 35020, pI: 7.90, NX(S/T): 3  
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTFVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVTVPVCRVPAKVPVVGKMATLHCQESGHPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIIGGIIGG  
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-30

#### **Transmembrane domain:**

amino acids 243-263

#### **N-glycosylation sites.**

amino acids 104-107, 192-195

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

#### **Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

#### **Tyrosine kinase phosphorylation site.**

amino acids 69-77

#### **N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267